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GenCore version 5.1.6
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- protein search, using sw model OM protein October 14, 2003, 08:34:01; Search time 21.8636 Seconds (without alignments) 94.378 Million cell updates/sec Run on:

US-09-931-700-2 76 1 YGGHQIYQFIDKD 13 Title:

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1107863 seqs, 158726573 residues Searched: 1107863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

| Sidos | Jacob | Color | Colo /SIDS1/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:\*/SIDS1/gcgdata/geneseg/genesegp-emb1/AA2003.DAT:\* /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:\* /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\* A\_Geneseq\_19Jun03:\* 22220 22220 22220 22220 22220 22220 22220 22220

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

|        |       | dР    |    |    |          |                    |
|--------|-------|-------|----|----|----------|--------------------|
| Result |       | Query |    |    |          |                    |
| No.    | Score |       | Le | DB | ID       | Description        |
| τ      | 92    | 100.0 | 13 | 18 | AAW25159 | Human preproadreno |
| 7      | 57    | 75.0  |    | 18 | AAW25160 | Human preproadreno |
| ľ      | 57    | 75.0  | 31 | 22 | AAB91762 | Adrenomedullin pep |
| 4      | 57    | 75.0  | 31 | 22 | AAE09827 | Human adrenomedull |
| Ŋ      | 57    | 75.0  | 40 | 22 | AAB91768 | Adrenomedullin pep |
| 9      | 57    | 75.0  | 50 | 22 | AAE09819 | Rat adrenomedullin |
| 7      | 57    | 75.0  | 52 | 22 | AAB75110 | Human adrenomedull |
| 80     | 57    | 75.0  | 52 | 22 | AAB91759 | Adrenomedullin pep |
| 6      | 57    | 75.0  | 52 | 22 | AAB91765 | Adrenomedullin pep |

|          | lrenomedul | Glycine extended h | Glycine extended a | Universal stress p | Linker peptide-adr | UspA(1-57)-(A)-(GS | UspA(1-56)-(DD)-(G | Universal stress p | _   | 4    | Universal stress p | Thioredoxin-(GSGSG | Human adrenomeduli | Rat adrenomedulin | Human adrenomedull | Rat adrenomedullin | Adrenomedullin, in | Porcine adrenomedu |      | Universal stress p | Adrenomedullin pep | aemic | E    | on. |     | Arabidopsis thalia | S: Lavendulae MmcA | H. pylori cytoplas | Adrenomedullin pep | Lactococcus lactis | Staphylococcus aur | Human polypeptide, | Human Plexin-B2. | plexin- | Novel human diagno |
|----------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----|------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|------|--------------------|--------------------|-------|------|-----|-----|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|---------|--------------------|
| AAE09818 |            |                    | AAB75112           | ABJ1               | AAB7               | AAB7               |                    | ABJ1               |     |      |                    | AAB7511            |                    |                   | AAB6034            |                    |                    | AAB4969            |      |                    | AAB9176            |       | ·    |     |     |                    | ·                  |                    |                    |                    |                    | AAM93421           |                  |         | ABG21017           |
|          |            |                    |                    |                    |                    |                    |                    |                    |     | 22   |                    |                    |                    |                   |                    |                    |                    |                    |      |                    |                    |       |      |     |     |                    |                    |                    |                    |                    |                    |                    |                  |         |                    |
| 52       | 52         | 53                 | 53                 | 53                 | 62                 | 120                | 120                | 120                | 120 | 147  | 147                | 170                | 185                | 185               | 185                | 185                | 185                | 188                | 188  | 206                | 53                 | 184   | 986  | 757 | 166 | 176                | 514                | 2440               | 37                 | 185                | 519                | 716                | 1838             | 1849    | 1870               |
| 75.0     | ď.         | 5                  | 5                  | 5.                 | رى<br>س            | 5                  | S.                 | 'n.                | 'n. | 75.0 | īÜ.                | ď.                 | ď.                 | 75.0              |                    |                    | 10                 |                    | 75.0 | ın.                |                    | 7     | ď    | œ.  | φ.  | 6                  | 7                  | 7.                 | ₹.                 | ω.                 | e,                 | 52.6               | ά.               | ď       | o.                 |
| 57       | 57         | 57                 | 57                 | 57                 | 27                 | 57                 | 57                 | 57                 | 57  | 57   | 57                 | 57                 | 57                 | 57                | 22                 | 57                 | 57                 | 57                 | 57   | 57                 | 51                 | 51    | 45.5 | 45  | 4.5 | 45                 | 44                 | 44                 | 41.5               |                    | 41                 | 40                 | 40               | 40      | 40                 |
| 10       | 11         | 12                 | 13                 | 14                 | 15                 | 16                 | 17                 | 18                 | 19  | 20   | 21                 | 22                 | 23                 | 24                | 25                 | 26                 | 27                 | 28                 | 29   | 30                 | 31                 | 32    | 33   | 34  | 35  | 36                 | 37                 | 38                 | 33                 | 40                 | 41                 | 42                 | 43               | 44      | 45                 |

## ALIGNMENTS

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Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone; skin; blood related; disease; type II diabetes; preeclampsia; neurotransmission regulation; allergy; mast cell degranulation; antibacterial; antifungal; wound repair.
                                                                                                                                                                                                                    /note= "residues 122-131 of preproadrenomedullin with Tyr-Gly-Gly attached at N-terminus"
                                                                                       Human preproadrenomedullin derived immunogen, PO71.
                                                                                                                                                                                             Location/Qualifiers
                     AAW25159 standard; peptide; 13 AA.
                                                                                                                                                                                                                                              13
/note= "amidated"
                                                                                                                                                                                                                                                                                                                             96WO-US13286.
                                                                                                                                                                                                                                                                                                                                                   96US-0013172.
                                                                   (first entry)
                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                    12-MAR-1996;
18-AUG-1995;
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                              16-AUG-1996;
                                                                 08-DEC-1997
                                                                                                                                                                                                                                                                                WO9707214-A1
                                                                                                                                                                                                                                                                                                       27-FEB-1997.
                                           AAW25159;
                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                  Key
RESULT 1
            AAW25159
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Best_Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                 WPI; 1997-165298/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200069900-A2.
   12-MAR-1996;
18-AUG-1995;
30-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-1999;
15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB91762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adrenomedullin (AM) peptides P070, P071, P072 and PAMP-20
were used for the production of anti-AM antibodies (Ab). P070 represents
preproAM amino acids (as) 34.41 with the sequence Tyr-Tyr attached at
the N-terminus, P071 represents preproAM as 122-131 with the sequence
Tyr-Gly-Gly attached at the N-terminus, P072 represents preproAM as
116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
for the prevention and/or treatment of cancers, e.g. adrenal, nervous
system, lung, colon, ovarian and breast cancer by inhibiting cell
growth. They are also useful for regulating insulin secretion and blood
glucose metabolism and therefore for treating and/or preventing diabetes
type II. They may be used for the diagnosis or treatment of conditions
relating to pregnancy e.g. precelampsia. The Ab are also useful
areas of the central nervous system; (ii) lessening or inhibiting mast
cell degranulation and hence reducing the effects of an allergic
response; (iii) inhibiting or preventing bacterial and fungal growth (to
treat infection); (iv) faculitating wound healing; and (v) promoting
crypt and bone development.
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                                                                                                                                            Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used in the diagnosis and treatment of type II diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone; skin; blood related; disease; type II diabetes; preeclampsia; neurotransmission regulation; allergy; mast cell degranulation; antibacterial; antifungal; wound repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "residues 116-146 of preproadrenomedullin"
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T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human preproadrenomedullin derived immunogen, PO72.
                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25160 standard; peptide; 31 AA.
                                                                                                                                                                                        Claim 1; Page 43; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "amidated"
                                                           Cuttitta F, Gray K, Hook W,
Miller MJ, Unsworth EJ, Walsh
95US-0002936.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                          WPI; 1997-165298/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AA;
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30-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25160;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20 were used for the production of anti-AM antibodies (Ab). PO70 represents preproAM amino acids (as) 34-41 with the sequence Tyr-Tyr attached at the N-terminus, PO71 represents preproAM as 122-131 with the sequence Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM as 116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful for the prevention and/Or treatment of cancers, e.g. aftenal, nervous system, lung, colon, ovarian and breast cancer by inhibiting cell growth. They are also useful for regulating insulin secretion and blood glucose metabolism and therefore for treating and/or preventing and blood glucose metabolism and therefore for treating and/or preventing adiabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type II. They may be used for the diagnosis or treatment of conditions relating to pregnancy e.g. preeclampsia. The Ab are also useful for the following: (i) regulating neurotransmission or neuron growth in areas of the central nervous system; (ii) lessening or inhibiting mast cell degranulation and hence reducing the effects of an allergic response; (iii) inhibiting or preventing bacterial and fungal growth (to treat infection); (iv) facilitating wound healing; and (v) promoting organ and bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                        Martinez A;
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                                                                                                                                                                                                               Macri C,
T;
                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB91762 standard; Peptide; 31 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 43; 106pp; English.
                                                                                                                                                                                                               Cuttitta F, Gray K, Hook W,
Miller MJ, Unsworth EJ, Walsh
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99US-0153406.
99US-0159783.
95US-0002514.
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WO200069900-A2.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                         AAB91768;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                            RESULT 5
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 X E E X E X D D D D D D D D D X S
                                                                                                                                            comprising a therapeutically actives amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/Mydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half if its) and specificity as bonding to large molecules decreases in the action of the present peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                  Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                       The present invention describes a modified therapeutic peptide (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
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                       Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 31;
0.006;
hes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                Disclosure; Page 499-500; 733pp; English.
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                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE09827 standard; peptide; 31 AA.
                       Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human adrenomedullin peptide #2.
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                           7 HQIYQFTDKD 16
(CONJ-) CONJUCHEM INC
                        Ezrin AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-564216/63.
                                           WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                 31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                       Bridon DP,
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                                                                                                                                                                   The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact cells either in vitro or in vivo to inhibit the effect of CGRP adrenomedullin peptide.
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Vasoactive peptides useful for inhibiting calcitonin gene related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 57; DB 22; Length 31; 100.0%; Pred. No. 0.006; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adrenomedullin peptide (AM) SEQ ID NO:944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB91768 standard; Peptide; 40 AA.
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                                                                                                     Claim 5; Column 6; 24pp; English.
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99US-0153406.
99US-0159783.
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Best Local Similarity luv.v.
10, Conservative
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                                       peptide receptor activity
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HQIYQFIDKD 13

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(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
CGRP-receptor identification; adrenomedullin.
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                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                      75.0%; Score 57; DB 22; Length 40 100.0%; Pred. No. 0.008; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          AAE09819 standard; peptide; 50 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abel PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0070504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat adrenomedullin peptide
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                        HQIYQFTDKD
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                                                                                                                                                                                                        40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-JUL-2001
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                                                                                                                                                                                                        Sequence
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The present invention describes a method (MI) for producing darenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host
                                                                                                                          Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                Mitsushima K;
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                                                                                                                                                                                                                                                                                                                                                Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 45; 75pp; Japanese.
             AAB75110 standard; Protein; 52 AA.
                                                                                               Human adrenomedullin (AM) protein.
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100.0%; Pre
0; '
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                                                                                                                                                                                                                                                        10-OCT-2000; 2000WO-JP07023.
                                                                                                                                                                                                                                                                                      99JP-0294147
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                             Takimoto A, Mitsuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 HQIYQFTDKD 13
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                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-282044/29.
N-PSDB; AAH19806.
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Best Local Similarity
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                                                                                                                                                                                                WO200127310-A1
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                    15-OCT-1999;
                                                                    31-JUL-2001
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                                         AAB75110;
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AAB75110
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Gaps

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Indels

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DB 22; Length 50; 0.01;

75.0%; Score 57; DB 100.0%; Pred. No. 0.0 cive 0; Mismatches

Best Local Similarity 100. Matches 10; Conservative

Query Match

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us-09-931-700-2.rag

2000WO-US13576.

99US-0134406

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WO200069900-A2
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                                                                           17-MAY-2000;
                                                                                                   17-MAY-1999;
                                                                                                                10-SEP-1999;
15-0CT-1999;
                                                  23-NOV-2000
 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                           comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (III) and a less therapeutically active amino acid region (IV), which covalently and sutto. The set therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not sultable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half intecellular uptake and interference with physiological processes. AAB90829 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                         Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                   present invention describes a modified therapeutic peptide (I)
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                                                                                                                                                                                                                                        Milner PG, Holmes DL, Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 22; Length 52; 100.0%; Pred. No. 0.011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 498; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB91765 standard; Peptide; 52 AA.
                                                                                                                                                              99US-0134406.
99US-0153406.
99US-0159783.
                                                                                                                                       17-MAY-2000; 2000WO-US13576.
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                                                                                                                                                                                                                                         Ezrin AM,
                                                                                                                                                                                                               (CONJ-) CONJUCHEM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
ses 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 AA;
                                                                                    WO200069900-A2
                                                  Homo sapiens.
                                                                                                                                                                         10-SEP-1999;
15-0CT-1999;
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                                                                                                              23-NOV-2000
                                                                                                                                                                                                                                         Bridon DP,
                                                              Synthetic.
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases in the activity are and interference with physiological processes. ARB90829 to AAB92441 represent invention.
                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                                                                                                                                              Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 57; DB 22; Length 52; 100.0%; Pred. No. 0.011; Live 0; Mismatches 0; Indels
                                                                                                                                                                              Milner PG, Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 501; 733pp; English.
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99US-0153406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 HQIYQFTDKD 13
                                                                                                                                                                              Bridon DP, Ezrin AM,
                                                                                                       (CONJ-) CONJUCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HQIYQFTDKD
                                                                                                                                                                                                                                                 WPI; 2001-112059/12.
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es 10; Conserv
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us-09-931-700-2.rag

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present sequence is that of human adrenomedullin, a potent
                                                                                                                                                                                    4 HOIYQFTDKD 13
                                                                                                                                                                                                   28 HQIYQFTDKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 A.A.;
                                                                                                                                 52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinant host
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                                                                                                                                                                                                                                                                                                                                                          WO200127310-A1.
                                                                                                                                                                                                                                                                               31-JUL-2001
                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                 Sequence
                                                                                                                                                                                                                                                              AAB75111;
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                                                                                                                                                                  Matches
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                                                                                                                            calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. cells either in vitro or isolate CGRP receptors or with intact binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New modified human calcitonin peptide having reduced aggregation, useful for the treatment of Paget's disease, hypercalcemia and/or
                                                                          Vasoactive peptides useful for inhibiting calcitonin gene related
                                                                                                                                                                                                                                                     ö
                                                                                                                      The invention relates to antagonists of the vasoactive peptide
                                                                                                                                                                                                                                   DB 22; Length 52; 0.011;
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Adrenomedullin; human; protein engineering; solubility; aggregation; hypotensive; vasodilator; cyclic.
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                                                                                                                                                                                                                                  75.0%; Score 57; DB 100.0%; Pred. No. 0.0
                                                                                                    Claim 5; Column 25-26; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
16..21
                                                                                                                                                                                                                                                                                                                             ABP55104 standard; Peptide; 52 AA
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        98US-0070504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISIS-) ISIS INNOVATION LID
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                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                     peptide receptor activity
                                                                                                                                                                                                                            Query Match 100.
                         (UYCR-) UNIV CREIGHTON.
                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                              Human adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobson CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-046916/04.
                                                                                                                                                                                                                                                                    4 HQIYQFTDKD
                                                          WPI; 2001-564216/63
                                        Saha S,
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             osteoporosis
        30-APR-1998;
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                                        Smith DD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zurdo J,
                                                                                                                                                                                                                   Seguence
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The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
hypotensive and vasodilator. The invention provides modified callitonin and related peptides, such as adrenomedullin, that have at least 70% identity to the native form but are modified such that the tendency of the peptide to aggregate is reduced. Preferred regions for modification include those for which the peptide is polymorphic amongst different species, which increase the propensity of the peptide to form local interactions of the alpha-helical type, or which reduce the number of hydrophobic residues or increase the net charge of the peptide. When aggregation is reduced or prevented, lower doses of the drug can be used. Side-effects and undesired responses are minimised by retaining high sequence identity to the human peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 52; 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. No. 0.0
tive 0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB75111 standard; Protein; 53 AA.
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The invention comprises a novel fusion peptide which contains an Escherichia coli universal stress protein (UspA), a linker peptide and a target peptide. The fusion protein is cleavable by a protease. The fusion peptide of the invention is useful for the efficient large scale production of peptides. The present amino acid sequence represents a protein that was used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                              universal stress peptide; UspA; linker peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linker peptide-adrenomedullin (AM) precursor protein.
                                              Universal stress protein A (uspA)-related protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.0%; Score 57; DB 24;
100.0%; Pred. No. 0.011;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 30; 49pp; Japanese.
                                                                                                 large scale peptide production.
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                                                                                                                                                                                                                                                                     10-APR-2001; 2001JP-0111088.
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            27-FEB-2003 (first entry)
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                 Fusion peptide;
                                                                                                                                                                 WO200283907-A1
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                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by cleavage
                                                                                                                                                                                                     24-OCT-2002.
                                                                                                                                                                                                                                                                                                                                          Mitsuda Y;
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                                                                                                                                                                                                                                                                                                                                       Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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              Length 53;
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                                                0; Indels
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                                                                                                                                                                                                                                                                                                          Glycine extended adrenomedullin (AM-gly) protein.
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Pred. No. 0.011;
              DB 22;
0.011;
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100.0%; Pred. No. v...
0; Mismatches
                                                 Mismatches
                Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 47; 75pp; Japanese.
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                                                                                                                                                                                                       AAB75112 standard; Protein; 53 AA.
     75.0%; Scor.
100.0%; Pre
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                                                                                                                                                                                                                                                                       (first entry)
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                 Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                     4 HQIYQFIDKD 13
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N-PSDB; AAH19808.
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                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
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RESULT 13

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ABJ18665

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Gaps

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Length 53; 0; Indels

(SHIO ) SHIONOGI & CO LID.

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The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host \,\cdot\,
                                                             Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
                                                                                                                                                                                                                                                   Claim 20; Page 48; 75pp; Japanese.
                                                                                                  WPI; 2001-282044/29.
N-PSDB; AAH19809.
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62 AA; Seguence

Gaps ; Query Match 75.0%; Score 57; DB 22; Length 62; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels

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4 HQIYQFIDKD 13 δλ Op

Search completed: October 14, 2003, 08:38:46 Job time: 22.8636 secs

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                                                                                                                          October 14, 2003, 08:37:31; Search time 8.56818 Seconds (without alignments) 64.196 Million cell updates/sec
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Sequence 3, A
Sequence 4, A
Sequence 5, A
Sequence 23,
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Sequence 15,
Sequence 7,
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Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-486-596A-1

US-09-004-713-1

US-08-233-389C-3

US-08-801-863-3

US-08-486-596A-3

US-09-004-713-3

US-09-280-501-17

US-09-266-965-116
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US-09-280-501-3
US-09-280-501-4
US-09-070-504-23
US-09-011-922A-3
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US-09-070-504-15
US-09-070-504-14
US-09-070-504-14
US-08-233-389C-1
US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -922A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -501-9
-501-6
-501-8
                                                                                                                                                                                                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-280-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-280
                                                                                    protein search, using sw model
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                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                         1 YGGHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 0
length: 2000000000
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76
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Match Length
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Maximum DB seq
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                                                                                      OM protein
                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database
                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
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| Sequence 4347, Ap | US-09-134-001C-4347  | 4 | 514  | 47.4 | 36   | 45 |
|-------------------|----------------------|---|------|------|------|----|
| Sequence 2, Appli | US-09-581-831-2      | 7 | 484  | 47.4 | 36   | 44 |
| Sequence 118, App | US-09-266-965-118    | 4 | 470  | 47.4 | 36   | 43 |
| Sequence 2, Appli | US-09-333-423-2      | m | 347  | 47.4 | 36   | 42 |
| Sequence 24398, A | US-09-252-991A-24398 | 4 | 291  | 47.4 | 36   | 41 |
| Sequence 3675, Ap | US-09-107-532A-3675  | 4 | 231  | 47.4 | 36   | 40 |
| Sequence 4, Appli | US-07-998-289B-4     | m | 196  | 47.4 | 36   | 39 |
| Sequence 12, Appl | US-08-851-567B-12    | 4 | 2504 | 48.7 | 37   | 38 |
| Sequence 53, Appl | US-08-851-567B-53    | 4 | 1844 | 48.7 | 37   | 37 |
| Sequence 75, Appl | US-09-599-360B-75    | 4 | 302  | 48.7 | 37   | 36 |
| Sequence 6073, Ap | US-09-107-532A-6073  | 4 | 418  | 50.0 | 38   | 35 |
| Sequence 5962, Ap | US-09-107-532A-5962  | 7 | 396  | 50.7 | 38.5 | 34 |
| Sequence 2, Appli | US-09-306-881-2      | m | 374  | 50.7 | 38.5 | 33 |
| Sequence 8, Appli | US-09-368-169-8      | m | 686  | 51.3 | 39   | 32 |
| Sequence 21838, A | US-09-252-991A-21838 | 7 | 433  | 51.3 | 39   | 31 |
| Sequence 25900, A | US-09-252-991A-25900 | 4 | 157  | 52.6 | 40   | 30 |
| Sequence 241, App | US-09-634-238-241    | 4 | 317  | 53.9 | 41   | 29 |
| Sequence 19737, A | US-09-252-991A-19737 | 4 | 264  | 53.9 | 41   | 28 |
|                   |                      |   |      |      |      |    |

### ALIGNMENTS

```
Sequence 2, Application US/09011922A
; Sequence 2, Application US/09011922A
; Patent No. 6320020;
; GENERAL INFORMATION:
   APPLICANT: Cuttitta, Frank; Martinez,
   APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
   APPLICANT: Aren; Mailliam; Walsh, Thomas; Grey,
   APPLICANT: Karen; Marti, Charles
   TITLE OF INVENTION: Functional Role of
   TITLE OF INVENTION: Product (PAMP) in Human Pathology and
   TITLE OF INVENTION: Physiology
   NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: ASCII
CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION NUMBER: US/60/013,172
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
PRIOR APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY-AGENT INFORMATION:
NAME: LAGIN INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 759-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leslie A. Serunian
                                                                                                                                                                                                                                                                                                                                                                                                                                  : 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
RESULT 1
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Sequence 3, Appli Sequence 17, Appl Sequence 116, App

Appli

Sequence Sequence Sequence Sequence

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RESULT 5
US-09-280-501-3
                                                                                                                                                                                                              RESULT 4
US-09-280-501-2
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LENGIH: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                        Query Match
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Sequence 1, Application US/09280501

Sequence 1, Application US/09280501

Sequence 1, Application US/09280501

GENERAL INFORMATION:

APPLICANT: Coroper, Garth James Smith

APPLICANT: Corolesh, Jaillian

TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH

TITLE OF INVENTION: ADRENOMEDULIN OR ADRENOMEDULLIN AGONISTS

FILE REFERENCE: 08987-005501

CURRENT APPLICATION NUMBER: US/09/280,501

CURRENT FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: 08/634,562

PRIOR FILING DATE: 1996-04-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULIN OR ADRENOMEDULIN AGONISTS
FILE REFERENCE: 08997-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT APPLICATION NUMBER: 08/094.280
PRIOR FILING DAIE: 1996-04-18
PRIOR FILING DAIE: 1996-04-18
                                                                                                                                                                                                            Query Match 100.0%; Score 76; DB 4; Length 13; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.0%; Score 57; DB 4; Length 13; 100.0%; Pred. No. 0.0016; Live 0; Mismatches 0; Indels
                                                                                                                 ; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
10X-09-280-501-15
5 Sequence 15, Application US/09280501
7 Patent No. 6440421
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                1 YGGHQIXQFTDKD 13
                                                                                                                                                                                                                                                                                                                                        1 YGGHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100 nes 10; Conservative
                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HOIYOFTDKD 10
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CORGANISM: Homo sapiens
US-09-280-501-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-09-280-501-15
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LENGTH: 26
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LENGIH: 13
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reld, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1996-04-18
75.0%; Score 57; DB 4; Length 26; 100.0%; Pred. No. 0.0033; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 4; Length 27; 100.0%; Pred. No. 0.0034; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.0%; Score 57; DB 4; Length 28; 100.0%; Pred. No. 0.0035; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 27
                                                                                                                                                                              ; Sequence 2, Application US/09280501; Patent No. 6440421
                 Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Conservative
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                                                                4 HQIYQFTDKD 13
                                                                                               2 HQIYQFIDKD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) ORGANISM: Homo sapiens
US-09-280-501-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charliam; Walsh, Thomas; Grey,
ATPLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
    PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%; Score 57; DB 3; Length 31; 100.0%; Pred. No. 0.0039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                    SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
                                                                                      SSEE: Mueting, Raasch & Gebhardt, P.A.
F: 119 No. 6268474th Fourth Street
Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. w-
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MCCOTMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09011922A; Patent No. 6320022; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                       COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-non-software
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Conservative
TITLE OF INVENTION: PER TITLE OF INVENTION: SUF NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                  ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
US-09-011-922A-3
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                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                 STREET:
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Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
ITILE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
ITILE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                            APPLICANT: Cooper, Garth James Smith
APPLICANT: Cooper, Garth James Smith
APPLICANT: Cornish, Jillian
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREAPMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMER: 1999-03-30
PRIOR FILLING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 4
LENGTH: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%; Score 57; DB 4; Length 29; 100.0%; Pred. No. 0.0037; tive 0; Mismatches 0; Indels
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Patent No. 6268/74
GENERAL INFORMATION:
APPLICANT: Saha, Shankar
APPLICANT: Saha, Shankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/09280501
; Patent No. 6440421
                                                                 Sequence 4, Application US/09280501
Patent No. 6440421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abel, Peter W.
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Matches 10; Conservative
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US-09-280-501-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                 GENERAL INFORMATION:
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US-09-280-501-5
                           RESULT 6
US-09-280-501-4
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LENGTH: 30
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APPLICATION NUMBER: US/60/002,936
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APPLICANT: Otttitte, Frank, Martinez,
APPLICANT: Alfred; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfred; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Arzen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
IN-SUGGOOO2,514
FILING DATE:
IN-SUGGOOO2,514
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER:
INLING DATE:
APPLICATION NUMBER:
INLING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
STANTONNEY, AGENT INFORMATION:
NAME:
LESLIG A. SETUNIAN
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATIO
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION UNBER: 05/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
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ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Partent No. 6320022
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ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 754-6849
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 10; Conservative
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Patent No. 6440421

GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Cooper, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic homolog of two-thirds of the intact AM peptide
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                                                                                                                                                                                NAME: Leglie A. Serunian
REGISTRATION NUMBER: 35,353
REGISTRATION NUMBER: 2026-4202US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 756-4800
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/13286
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
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                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31 amino acids
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US-09-280-501-9
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OTHER INFORMATION:
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Best Local Similarity
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Gaps
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                                                                                                                                                                                                                 75.0%; Score 57; DB 4; Length 40; 100.0%; Pred. No. 0.0051; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.0%; Score 57; DB 3; Length 50; 100.0%; Pred. No. 0.0065; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REGARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Reasch & Gebhardt, P.A.
ADDRESSEE: Mueting, Reasch & Gebhardt, P.A.
GITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180.00020101
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 14, 2003, 08:41:21 Job time: 9.56818 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Sha, Shankar
APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MCCOFMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 amino acids
                                                                                                                                                                                                                 Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 HQIYQFIDKD 13
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                                                                                                                                                                                                                                                                                                                  4 HQIYQFTDKD 13
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                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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US-09-070-504-15
                                                                                                                                                                    US-09-280-501-11
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                                                                     SEQ ID NO 11
LENGTH: 40
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                                                                                                                       TYPE: PRT
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Patent No. 6440421

GENERAL INFORMATION

APPLICANT: Corper, Garth James Smith
APPLICANT: Cornish, Jillian

TITLE OF INVENTION: ARRENDENT OF BONE DISORDERS WITH

TITLE OF INVENTION: ARRENDENT OF BONE DISORDERS

FILE REPERENCE: 08 987 -00501

CURRENT APPLICATION NUMBER: U590-03-30

PRIOR FILING DATE: 1996-04-18

NUMBER OF SEQ ID NOS: 17

NUMBER OF SEQ ID NOS: 17

NUMBER OF SEQ ID NOS: 17
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
CURRENT APPLICATION UNMBER: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
IITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
IITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                75.0%; Score 57; DB 4; Length 38; 100.0%; Pred. No. 0.0049; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%; Score 57; DB 4; Length 40; 100.0%; Pred. No. 0.0051; tive 0; Mismatches 0; Indels
                                                                                                                FILE REFERENCE: 08987-005001
CURRENT PELLION NUMBER: 08/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PASKSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/09280501
Patent No. 6440421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens US-09-280-501-8
                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-280-501-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-280-501-8
                                                                                                                                                                                                                                                                                                                                                                                   US-09-280-501-6
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LENGTH: 40
                                                                                                                                                                                                                                                                                         SEQ ID NO 6
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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Page 1

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October 14, 2003, 08:40:27; Search time 26 Seconds (without alignments) 80.564 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600653 seqs, 161128416 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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76
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                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Sequence 2, Appli | Sequence 14, Appl | Sequence 23, Appl | Sequence 15, Appl | Sequence 14, Appl | Sequence 2, Appli | Sequence 116, App | Sequence 116, App | Sequence 2, Appli | Sequence 5230, Ap   | Sequence 306, App | Sequence 5238, Ap  | Sequence 6765, Ap  | Sequence 66, Appl |
|-------------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-------------------|--------------------|--------------------|-------------------|
| SUMMARIES<br>ID               | US-09-931-700-2   | US-09-931-700-14  | US-09-813-345-23  | US-09-813-345-15  | US-09-813-345-14  | US-10-197-954-2   | US-09-953-348-116 | US-10-267-255-116 | US-10-027-000-2   | US-08-781-986A-5230 | US-09-801-368-306 | US-09-738-626-5238 | US-09-738-626-6765 | US-09-895-298-66  |
| DB                            | - 60              | 0                 | 6                 | σ                 | 9                 | 15                | 12                | 15                | 15                | œ                   | 10                | 10                 | 10                 | 11                |
| *<br>Query<br>Match Length DB | 13                | 31                | 31                | 50                | 52                | 52                | 514               | 514               | 833               | 519                 | 1356              | 325                | 161                | 302               |
| %<br>Query<br>Match           | 100.0             | 75.0              | 75.0              | 75.0              | 75.0              | 75.0              | 57.9              | 57.9              | 57.9              | 53.9                | 51.3              | 50.0               | 48.7               | 48.7              |
| Score                         | 76                | 57                | 57                | 57                | 57                | 57                | 44                | 44                | 44                | 41                  | 39                | 38                 | 37                 | 37                |
| Result<br>No.                 | 1 40              | m                 | 4                 | Ŋ                 | 9                 | 7                 | 80                | 6                 | 10                | 11                  | 12                | 13                 | 14                 | 15                |

| Sequence 120, App<br>Sequence 2, Appli<br>Sequence 53, Appl<br>Sequence 8, Appli | Sequence 12, Appl<br>Sequence 32, Appl<br>Sequence 1062, Ap | Sequence 71, Appl<br>Sequence 630, App | Sequence 1075, Ap<br>Sequence 103, App | Sequence 4889, Ap<br>Sequence 1104, Ap | Sequence 10536, A | Sequence 12332, A<br>Sequence 12870, A | 1314            | Sequence 6, Appli | 9        | ģ              | 9              |                | 9              | ý              | 9        | ý          | ý             | o,            | o'          | Sequence 6, Appli |
|--|---|--|--|--|-------------------|--|-----------------|-------------------|----------|----------------|----------------|----------------|----------------|----------------|----------|------------|---------------|---------------|-------------|-------------------|
| US-10-254-074-2<br>US-10-254-074-2<br>US-10-242-056-5<br>US-09-817-514A-8        | US-10-242-056-<br>US-10-355-430-<br>US-09-764-868-          | US-09-955-999-7<br>US-09-764-868-6     | US-09-764-868-10<br>US-09-955-999-10   | OS<br>O                                | US-09-815-24      | -09-815-242-128                        | US-09-815-242-1 | US-10-137-870-    | US-10-14 | US-10-140-021- | US-10-140-274- | US-10-140-471- | US-10-140-807- | US-10-140-922- | US-10-14 | US-10-140- | US-10-141-698 | US-10-141-702 | US-10-141-7 | 2 US-10-142-421-6 |
|  | 222   |  | 44                                     |  | 0.0               |  |                 | 12                |          |                |                |                |                |                |          |            |               |               |             |                   |
| 345<br>688<br>1844<br>2504   | 2504<br>451<br>118  | 118                                    | 143                                    | 213                                    | 231               | 500                                    | 265             | 433               | 433      | 433            | 433            | 433            | 433            | 433            | 433      | 433        | 433           | 433           | 433         | 433               |
| 48.7<br>48.7<br>48.7   | 4 4 8 . 0<br>4 4 7 . 4                                      | 47.4                                   | 47.4                                   | 47.4                                   | 47.4              |  | 47.4            | 47.4              | 47.4     | 47.4           | 47.4           | 47.4           | 47.4           | 47.4           | 47.4     | 47.4       | 47.4          | 47.4          | 47.4        | 47.4              |
| 337<br>337<br>337  | 36.5<br>36.3  | 36<br>36                               | 36<br>36                               | 36<br>36                               | 36                | 30                                     | 36              | 36                | 36       | 36             | 36             | 36             | 36             | 36             | 36       | 36         | 36            | 36            | 36          | 36                |
| 116<br>118<br>119  | 22122   | 23<br>24                               | 25<br>26                               | 27                                     | 67                | 31                                     | 32              | 33                | 34       | 35             | 36             | 37             | 38             | 30             | 40       | 41         | 42            | 43            | 44          | 45                |

## ALIGNMENTS

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US-09-331-700-2

US-09-331-700-2

US-09-331-700-2

Sequence 2, Application US/0931700

Patent No. US20020055615Al

GENERAL INFORMATION:

APPLICANT: GUTITITA, FRANK

APPLICANT: MILLER, MAE JEAN

APPLICANT: MILLER, MAE JEAN

APPLICANT: MILLER, MAE JEAN

APPLICANT: MILLER, MAE JEAN

APPLICANT: MALLER, MAE JEAN

APPLICANT: UNSWORTH, EDWARD J.

APPLICANT: GREY, KAREN

APPLICANT: MACRI, CHERKLES

ITILE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and

ITILE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and

ITILE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology

FILE REFERENCE: 2026-420204

ITILE OF INVENTION: Physiology

FILE REFERENCE: 2026-420204

CURRENT FILING DATE: 1996-03-12

PRIOR FILING DATE: 1996-03-12

PRIOR FILING DATE: 1996-03-12

PRIOR FILING DATE: 1996-03-12

PRIOR FILING DATE: 1995-03-12

PRIOR FILING DATE: 1995-08-16

PRIOR FILING DATE: 1995-08-16

PRIOR FILING DATE: 1995-08-16

PRIOR FILING DATE: 1995-08-18

NUMBER OF SQ ID NOS: 17

SSD ID NO 2

LENGTH: 13

ITPE: PRI

CREATURE:

CREATURE:

TYPE: PRI

CREATURE:

CHER INFORMATION: POSCIPTION of Artificial Sequence: Peptide,

OTHER INFORMATION: PO71, YGG-PreproAM (amino acids 122-131)
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US-09-931-700-14
                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 14
LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MARTHRA, FRAND,
APPLICANT: MALEREDO
APPLICANT: MILLER, MAE JERNO
APPLICANT: MILLER, MAE JENN
APPLICANT: MILLER, MAE JENN
APPLICANT: HOW, WILLIAM
APPLICANT: GAEY, THOMAS
APPLICANT: GAEY, KAREN
APPLICANT: GAEY, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202046
TITLE OF INVENTION: Physiology
FILE REPERENCE: 2026-4202046
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT APPLICATION NUMBER: US/09/1922
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: US/00/02,336
PRIOR FILING DATE: US/00/02,336
PRIOR FILING DATE: US/00/02,514
PRIOR FILING DATE: USOF.AR-18
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0
                                                Length 13;
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                                                                                       Indels
                                         Query Match 100.0%; Score 76; DB 9; L. Best Local Similarity 100.0%; Pred. No. 1.6e-06; Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/09931700
Patent No. US20020055615A1
                                                                                                                                                                                                                                                                               Sequence 3, Application US/09931700
Patent NO. US200200055615A1
GENERAL INFORMATION:
APPLICANT: CUTTITTA, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MARTINES, ALFREDO
MILLER, MAE JEAN
UNSWORTH, EDWARD J.
HOOK, WILLIAM
WALSH, THOMAS
GREY, KAREN
MACRI, CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                         1 YGGHQIYQFTDKD 13
                                                                                                                              1 YGGHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CUTTITTA, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 HQIYQFTDKD 13
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US-09-931-700-14
                                                                                                                                                                                                                                          SULT 2
-09-931-700-3
US-09-931-700-2
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APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and TITLE OF INVENTION: Physiology FILE OF INVENTION: Physiology FILE REPERBORE: 2026-4202046

CURRENT APPLICATION NUMBER: US/09/931,700

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 09/011,922

PRIOR FILING DATE: 1996-02-17

PRIOR FILING DATE: 1996-08-16

PRIOR PLICATION NUMBER: US/60/013,172

PRIOR PRIOR FILING DATE: 1995-08-16

PRIOR FILING DATE: 1995-08-30

PRIOR FILING DATE: 1995-08-30

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 17

SOFTWARE: RELEASE NOS: 17

SOFTWARE: PARLOR NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smith, Derek D.
Saba, Shankar
Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814A1th Fourth Street
CIIY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITAL NUMBERS COMPATIBLE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <URKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 75.0%; Score 57; DB 9; I Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 10; Conservative 0; Mismatches 0
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REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEPAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-813-345-23; Sequence 23, Application US/09813345; Patent No. US20020068814A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 23
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Sequence 14, Application US/09813345
                  Patent No. US20020068814A1
GENERAL INFORMATION:
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SAHA, SHANKAT
ADEL, PETET W.
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 57; DB 9; Length 50; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
                                                                                                                                                                               Length 31;
                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814Alth Fourth Street
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: LBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                             Query Match 75.0%; Score 57; DB 9; I
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/813,345 FILING DATE: 20-Mar-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
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NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
                    LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 612/305-1228
                                   TYPE: amino acid
STRANDEDNESS: single
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  SEQUENCE CHARACTERISTICS
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Best Local Similarity 100.
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 HQIYQFTDKD 13
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RESULT 6 US-09-813-345-14

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Sequence 2, Application US/10197954
Publication No. US20030119021A1
GENERAL INFORMATION:
APPLICANT: Siddigi, Suhaib
APPLICANT: Siddigi, Suhaib
ITILE OF INVENTION: Capture Compounds, Collections Thereof
ITILE OF INVENTION: And Methods For Analyzing The Proteome And Complex
ITILE OF INVENTION: Compositions
FILE REFERENCE: 24743-2305
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/306,019
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             AFFLICANT. CHARACT Shankar Abel, Peter W.

IIILE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 57; DB 9; Length 52; 100.0%; Pred. No. 0.011; tive 0; Mismatches 0; Indels
                                                                                                                                                                            ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. US20020068814Alth Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: CUNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCCOIMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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PRIOR APPLICATION NUMBER: 60/314,123
PRIOR PILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
APPLICANT: Smith, Derek D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                              NUMBER OF SEQUENCES:
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Matches 10; Conserva
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US-08-781-986A-5230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 833
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                                                                                                                                                                                                                                                                                                                                             US-10-027-000-2
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                                                             TYPE: PRT
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                                                                                                                   Score 57; DB 15; Length 52;
Pred. No. 0.011;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sherman, David. H
APPLICANT: Sherman, David. H
APPLICANT: Wacoglu, Mustafa
APPLICANT: Varcoglu, Mustafa
APPLICANT: Tarcoglu, Mustafa
APPLICANT: Sheldon, Paul
TITLE OF INVENITON: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
FILE REFERENCE: 600.530US1
CURRENT APPLICATION NUMBER: US/09/953,348
CURRENT FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2000-03-10
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT MOO, Y
APPLICANT MOO, Y
APPLICANT He, M
APPLICANT He, M
APPLICANT Shelon, P
TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
FILE REFERENCE: 600.456031
CURRENT APPLICATION NUMBER: US/10/267,255
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR APPLICATION NUMBER: US 09/266,965
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1996-08-19
PRIOR FILING DATE: 1994-10-06
PRIOR FILING DATE: 1994-10-06
PRIOR FILING DATE: 1994-10-06
PRIOR FILING DATE: 1993-10-07
NUMBER OF SEQ ID NOS: 145
                                                                                                      75.0%; Sco...
100.0%; Pred. No. v. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 153
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 116
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                         ; Sequence 116, Application US/09953348; Publication No. US20030134398A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 116, Application US/10267255; Publication No. US20030124689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptomyces lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 80.0
Matches 8; Conservative
                                                                                                                   Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
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28 HQIYQFTDKD 37
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APPLICANT: Sherman, D
                                                       ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-267-255-116
                                                                                                                                                                                                                                                                                                                            US-09-953-348-116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-953-348-116
                                                                               US-10-197-954-2
SEQ ID NO 2
LENGTH: 52
                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                      RESULT 8
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Sequence 5230, Application US/08781986A

Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10027000

Publication No. US20030119006A1

GENERAL INFORMATION:
APPLICANT: Goedegebuur, Frits
APPLICANT: Ward, Michael
APPLICANT: Yao, Jiachael
TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids
TITLE OF INVENTION: Encoding the Same
FILE REFERENCE: GC696
CURRENT APPLICATION NUMBER: US/10/027,000
CURRENT PILING DATE: 2001-12-18
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FRASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.9%; Score 44; DB 15; Length 833; 53.8%; Pred. No. 34; 1. Indels 1; Mismatches 3; Indels
                                                                                                                                                          Score 44; DB 15; Length 514; Pred. No. 21; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 116 LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SORTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                           ; ORGANISM: Streptomyces lavendulae US-10-267-255-116
                                                                                                                                                               57.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | | :: | :| |||
682 YVGYRYYEFADKD 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YGGHQIYQFTDKD 13
                                                                                                                                                          Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 53.8
Matches 7; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                     2 GGHQIYQFTD 11
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Score 37; DB 10; Length 161;
Pred. No. 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 10;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
                                                                                                                                                                                            FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POLYNUCLECTIDES FILE REFERENCE: 249-125 CURRENT APPLICATION NUMBER: US/09/738,626 CURRENT FILING DAIE: 2000-12-18
                                                                                                                                                             APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6765
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Corynebacterium glutamicum US-09-738-626-5238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6765, Application US/09738626
Publication No. US20020197605A1
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6765
LENGTH: 161
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                 HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
                                                                                      YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
NAKAGAWA, SATOSHI
MIZOGUCHI, HIROS
ANDO, SEIKO
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HAYASHI, MIKIRO
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YOKOI, HARUHIKO
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SENOH, AKIHIRO
IKEDA, MASATO
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Best Local Similarity 50.0
6, Conservative
                                                     HAYASHI, MIKIRO
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13 GGPEVLEFTDID 24
                                                                         OCHIAI, KEIKO
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Best Local Similarity
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US-09-738-626-6765
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APPLICANT:
APPLICANT:
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APPLICANT:
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
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                                                                                                                                                                                                                                                                                            Score 41; DB 8; Length 519;
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 109272.147

CURRENT PELLING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US/09/801,368

PRIOR FILING DATE: 2000-01-09

PRIOR FILING DATE: 2000-01-19

PRIOR PLICATION NUMBER: US 60/160,587

PRIOR PRILCATION NUMBER: US 60/160,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
               NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERNICE/DOCKET NUMBER: PB248PP
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5230:
SEQUENCE CHARACTERISTICS:
LENGTH: 519 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5238, Application US/09738626; Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 306, Application US/09801368 Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 306
LENGTH: 1356
                                                                                                                                                                                                                                                                                          53.98;
66.78;
 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 66,/r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cali, Brian
Hecht, Peter
Holtzman, Doug
Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                       454 GGRQIGQFSSKD 465
                                                                                                                                                                                                                                                                                                                                                                     2 GGHQIYQFTDKD 13
                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salama, Sofie
Sherman, Amir
                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-781-986A-5230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Busby, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        496 HEVYEFTD 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 HQIYQFTD 11
                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-801-368-306
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                                                                                                                                                                                                                         TOPOLOGY:
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APPLICANT:
APPLICANT:
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1 LOCATION: (237)

2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-895-298-66
    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

Query Match

Best Local Similarity 50.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 3; Mismatches 3; Indels
    3; Indels
                                                                                                                                        RESULT 15
US-09-895-298-66

Sequence 66. Application US/09895298

Publication No. US20030078405A1

CENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION:
FILE REFERENCE: P2035P1

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT APPLICATION NUMBER: US/09/895,298

CURRENT APPLICATION NUMBER: O9/591,16

PRIOR FILING DATE: 2000-06-09

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR APPLICATION NUMBER: 60/113,006

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-16

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 231

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 66

LENGTH: 100 66
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: October 14, 2003, 08:53:16
Job time: 26 secs
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | |:| ||::
| 176 YPGLQVYTFTER 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YGGHQIYQFTDK 12
                                                                 62 GHRISNTTDKD 72
                                        3 GHQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
Matches
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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 14, 2003, 08:36:56; Search time 7.38636 Seconds (without alignments) 169.257 Million cell updates/sec Run on:

US-09-931-700-2 76 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YGGHQIYQFIDKD 13 Scoring table: Sequence:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

pir1:\* pir2:\* pir3:\* pir4:\* PIR 76:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|               |       | de    |        |    | SUMMARIES |                    |
|---------------|-------|-------|--------|----|-----------|--------------------|
| Result<br>No. | Score | Query | Length | DB | ID        | Description        |
| 1             |       | ıO    | 185    | 7  | JN0684    | adrenomedullin pre |
| 7             | 57    |       | 185    | ď  | JN0766    |                    |
| ٣             | 57    | 75.0  | 188    | 7  | S41600    | adrenomedullin - p |
| 4             | 51    | •     | 643    | ď  | 876069    | 1 prot             |
| ហ             | 45    |       | 776    |    | T02702    | hypothetical prote |
| 9             | 44    |       | 2231   |    | D71870    | Н                  |
| 7             | 42    | 55.3  | 280    |    | H70089    |                    |
| 80            | 42    |       | 324    |    | A87544    | Н                  |
| σ'n           | 42    |       | 350    |    | T21106    | Н                  |
| 10            | 42    | 55.3  | 563    |    | T09378    | hypothetical prote |
| 11            | 41    |       | 185    |    | C86705    | ч                  |
| 12            | 41    |       | 467    |    | T21690    | Н                  |
| 13            | 41    | 53.9  | 514    |    | D89775    | hypothetical prote |
| 14            | 40    |       | 146    |    | G83445    | conserved hypothet |
| 15            | 40    | 52.6  | 260    |    | H71979    | probable type II r |
| 16            | 40    | 52.6  | 275    |    | T32005    | hypothetical prote |
| 17            |       | 52.0  | 909    |    | T40556    |                    |
| 18            | 39    | 51.3  | 176    |    | B35697    | ĕ                  |
| 19            |       | 51.3  | 310    |    | н69986    | hypothetical prote |
| 20            | 39    |       | 444    | -  | E69130    | histidine-tRNA lig |
| 21            | 39    | 51.3  |        | 7  | JX0194    | prolyl oligopeptid |
| 22            | 39    | 51.3  | Н      | 7  | S51389    | ROM2 protein - yea |
| 23            | 38.5  | 50.7  |        | 7  | T22410    | hypothetical prote |
| 24            | 38    | 50.0  | 165    | 7  | F69819    | conserved hypothet |
| 25            | 38    | 50.0  | 254    | 7  | B70860    | probable enoyl-CoA |
| 26            | 38    | 50.0  | 257    | 7  | AH0859    | periplasmic fimbri |
| 27            | 38    | 50.0  | 264    | 7  | T23866    | hypothetical prote |
| 28            | 38    | 50.0  | 387    | 7  | T28402    | Fe                 |
| 29            | 38    |       | 391    | 7  | H89859    | hypothetical prote |

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0; Gaps

75.0%; Score 57; DB 2; Length 185; 100.0%; Pred. No. 0.014; Live 0; Mismatches 0; Indels

100.0%; Pred. No.

Query Match 75.0% Best Local Similarity 100.4 Matches 10; Conservative

| protein kinase, ca | protein kinase, ca | pectate lyase rela | pepT protein - Sta | ABC transporter, A | hypothetical prote | hypothetical prote | dextranase - Strep | alpha-amylase (EC | hypothetical prote | probable lipoprote | rfbT protein VC025 | oxidoreductase ypi | sugar phosphate nu | imidazoleglycerol- | hypothetical prote |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S17759             | T14335             | A96999             | S58356             | A95167             | H98032             | E84534             | T30291             | JS0101            | T26838             | AG0539             | HB2344             | B86817             | F90507             | E82238             | T29832             |
| 7                  | ~                  | C)                 | 7                  | ď                  | 7                  | ~                  | 7                  | C)                | ~                  | ~                  | 7                  | 7                  | 7                  | a                  | a                  |
|                    | Z,                 | 54                 | 71                 | 98                 | 98                 | 22                 | 37                 | 6                 | 5                  | 4                  | 7                  | 0                  | m                  | 7                  | 285                |
| 425                | 532                | 564                | ī                  | Ñ                  | 3                  | 9                  | 13.                | 56                | 70                 | 164                | 22                 | 25                 | 25                 | 25                 | 7                  |
| 50.0 425           |                    |                    |                    | 50.0               |                    |                    |                    |                   |                    |                    |                    |                    |                    |                    |                    |
| 38 50.0 425        |                    |                    |                    |                    | 8 50.0             |                    |                    | 49.3              | 48.7               |                    | 48.7               | 48.7               | 48.7               | 48.7               | 48.7               |

# ALIGNMENTS

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A; Nesatures: 1 100 NALLY
A; Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A; Accession: PN0548
A; Molecule type: protein
A; Residues: 22-41 < KIZ>
A; Kangawa, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, B; Chem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy A; Recession: JN0476; MUD:93249425; PMID:8387282
A; Molecule type: protein
A; Residues: 95-146 < KI3>
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-185 <18513
A; Residues: 1-185 <18513
A; Residues: 1-185 <18513
A; Experimental source: phecochromocytoma
A; Experimental source: phecochromocytoma
B; Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem Biophys. Res. Commun. 194, 720-725, 1993
A; Title: Cloning and characterization of CDNA encoding a precursor for human adrenome
A; Reference number: JN0684; MUID:93343928; PMID:7688224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F)1-21/Domain: signal sequence #status predicted <SIG>
F)22-41/Domain: proadrenomedullin #status predicted <PED>
F)22-41/Domain: proadrenomedullin #status predicted <PED>
F)22-41/Domain: proadrenomedullin #status verpenimal 20 peptide #status predicted <PAP>
F)25-146/Product: adrenomedullin #status experimental <AMAT>
F)47-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F)41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following F)110-115/Disulfide bonds: #status experimental
F)146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
                                                                                                                               C,Accession: JC2351; JN0684; PN0548; JN0476
R;Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A;Ittle: Genomic structure of human adrenomedulin gene.
A;Reference number: JC2351; MJID:94354869; PMID:8074714
                                                C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Gene: GDB:ADM
A)Cross-references: GDB:217070; OMIM:103275
A)Map position: 11pter-11qter
A)Introns: 33/2; 83/2
C)Keywords: amidated carboxyl end; blood pressure control; hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: pheochromocytoma C; Genetics:
adrenomedullin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-185 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JN0684
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A; Molecule type: DNA A: Residues: 1-643 <KAN>
A; Residues: 1-643 <KAN>
A; Residues: EMBL:D63999; GB:AB001339; NID:g1001396; PIDN:BAA10047.1; PID:d101
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Accession: T02702
A.Scession: T02702
A.Scession: T02702
A.Scession: T02702
A.Status: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Rosidues: 1-776 CR0U>
A.Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A.Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A.Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A.Cross-references: EMBL:AC005313; NID:g3548706
A.Cross-references: EMBL:AC005313; NID:g3548806
A.Cross-references: EMBL:AC005313; NID:g3548706
A.Cross-references:
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D71870
hypothetical protein jhp0928 - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
C.Species: Helicobacter pylori
C.Spariety: strain J99
C.Satze: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-oct-1999
C.Saccession: D71870
R.Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g03240 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T18E12.9
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C;Accession: T02702; A84446
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, I submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Status: preliminary
A:Status: preliminary
A:Molecule type: DNA
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A;Cross-references: GB:AE002093; NID:g3548806; PIDN:AAC34478.1; GSPDB:GN00139
C;Genetics:
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A;Note: T18E12.9
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Pred. No. 0.61;
2; Mismatches 1; Indels
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                                                                                                                                                                                           A; Reference number: S74322; MUID: 97061201; PMID: 8905231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.1
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          447 GHEIYQYTDPD 457
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84 GGHQIGHFSDSD 95
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A; Status: preliminary
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A; Map position: 2
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C.Keywords: amidated sequence #status predicted <SIG>
F.1-21/Domain: signal sequence #status predicted <PED>
F.22-18/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F.32-41/Product: adrenomedullin #status predicted <AMT>
F.94-143/Product: adrenomedullin #status predicted <AMT>
F.41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
F;143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                               C;Species: Rattus norregicus (Norway rat)
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C;Accession. JN0766; PN0610
R;Sakata, J.; Shinnokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T Risakata, J.; Shinnokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T A;Title: Molecular Cloning and biological activities of rat adrenomedullin, a hypotensiv A;Reference number: JN0766; MUID:93384621; PMID:7690563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 22-41 <SA2>
C;Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complète amino acid sequence of porcine adrenomedullin and cloning of cDNA enco
A; Reference number: S41600; MUID:94139945; PMID:8043068
A; Accession: S41600
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C;Species: Sus scrofa domestica (domestic pig)
C;Accession: S41600
B;Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
PEBS Lett. 338, 306-310, 1994
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A,Variety: Pcc 6803
C'bate: 25-Apr.1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C'Accession: S76069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 188;
0.014;
hes 0; Indels
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Best Local Similarity 100.(
Matches 10; Conservative
                                                                                                                                                                                                                                                                                       adrenomedullin precursor - rat
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Matches 10; Conservative
                                                               119 HQIYQFIDKD 128
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                       13
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                       HQIYQFTDKD
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A; Residues: 1-185 <SAK>
A; Accession: PN0610
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A; Residues: 1-188 <KIT>
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55.3%; Sco.
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20 YNGRKIFDFTERD 32
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A; Accession: T04999
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Best Local Similarity
``haq 6; Conserva
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Best Local Similarity
                                                                                                                                                                                        A; Molecule type: DNA A; Residues: 1-324 <STO>
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H70089
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M; Alloni, G; Azevedo, V; Berter
C; Bron, S; Broullet, S; Bruschi, C,V; Caldwell, B; Capuano, V; Carter, N.M; Chc
A; Brulich, S.D; Emmerson, P.T.; Entlan, K.D; Errington, J; Fabret, C; Ferrari, E
Nature 390, 249-256, 1997
R; Kunter, B; Koningstedin, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Hullo, M; Krotter, P; Koningstedin, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardinois, A; Authors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masudel, S; Muthors: Lauber, J; Lazarevic, V; Lee, S.M; Levine, A; Liu, H; Masudel, S; Authors: Schleich, S; Schroeter, B; Rose, M; Sadaie, Y; Sato, T; Scanlon, A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekiguchi, J; Sekwaka, A; Seror akeuthi, M; Tamakoshi, A; Tanaka, T; Perpstra, P; Tognoni, A; Tosato, V; Toshida, R; Altile: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Reference number: A69580; MUID:98044033; PMID:9384377
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Reference number: A71800
A;Status: preliminary
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R;Nerman, W.C.; Peldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
                                                                                                                                                                                                                                                                                         GB:AE001439; NID:94155505; PIDN:AAD06506.1; PID:9415550
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A;Experimental source: strain 168
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A;Molecule type: DNA
A;Residues: 1-280 <KUN>
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C;Superfamily: Bacillus subtilis hypothetical protein yycl
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 44; DB Pred. No. 40; 2; Mismatches
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A:Molecule type: DNA
A:Residues: 1-2231 <ARN>
A:Cross-references: GB:AE001522; G
A:Experimental source: strain J99
C:Genetics:
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Matches 8; Conserv
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A.Reference number: 219375
A.Accession: T21106
A.Status: praininary; translated from GB/EMBL/DDBJ
A.Status: praininary; translated from GB/EMBL/DDBJ
A.Rolecule type: DNA
A.Residues: 1-350 <WIL>
A.Cross-references: EMBL: 269635; NID: 91200023; PIDN: CAA93458.1; GSPDB: GN00022; CESP: FA: Experimental source: clone F19B6
C.Genetics:
A.Genetics: A.Genetics: A.Genetics: CESP: F19B6.3
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C;Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolc
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C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 01-Dec-2000
C.Daccession: T03378; T04999
R.Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K. submitted to the Protein Sequence Database, June 1999
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R; Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.F. submitted to the Protein Sequence Database, April 1998
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F19B6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21106
R:Thomas, K.
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A; Molecule type: DNA
A; Residues: 1-563 < BEV>
A; Cross-references: EMBL: AL078620; GSPDB: GN00062; ATSP: F23K16.250
                                                                                                                                                                                                                                                                                                                                                                          55.3%; Score 42; DB 2; Length 324; Llarity 50.0%; Pred. No. 11; Conservative 2; Mismatches 4; Indels
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A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUD:21173698; PMID:11259647 A;Accession: A87249; MUD:21173698; PMID:11259647 A;Status; preliminary
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A;Residues: 444-563 <BE2>
A;Cross-references: EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
C;Genetics:
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Pred. No.
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hypothetical protein [imported] - Staphylococcus aureus (strain N315)
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C, Genetics:
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Matches 7; Conservative
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Best Local Similarity
Matches 8; Conserva
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A; Cross-references: GB:AE005176; PID:g12723547; PIDN:AAK04741.1; GSPDB:GN00146
A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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**Macrons**. 20,73; 212/3; 212/3; 212/3; 256/3; 365/3

**Molecule type: DNA
**A.Molecule type: DNA
**A.Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein F33A8.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T21690
R;Matthews, L.
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                      Length 563;
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                                                                                                                                                                                            Score 42; DB 2
Pred. No. 21;
3; Mismatches
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Pred. No. 9.3;
0; Mismatches
                                                                                                                                                                                            55.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.9%;
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                                                                                                                                                                                                                                                                                                                                                                     2 GGHQIYQFTDKD 13
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YGGHQIYQFTDK 12
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A;Map position: 4
A;Introns: 118/3; 502/3
A;Note: T19P19:10
                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: DNA
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RESULT 13 D89775

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Conserved hypothetical protein PA1607 [imported] - Pseudomonas aeruginosa (strain PAO C; Species: Pseudomonas aeruginosa (c; Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 (3) Accession: G83445 (83445 R. Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Nature 406, 959-964, 2000
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A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-146 <STO>
A;Cross-references: GB:AE004588; GB:AE004091; NID:99947563; PIDN:AAG04996.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable type II restriction enzyme - Helicobacter pylori (strain J99)
G.Species: Helicobacter pylori
A.Variety: strain J99
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-oct-1999
G.Accession: H71979
F.Alm, R.A.: Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D. Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.
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Jypourelucal pluelin imported - Staphylococcus aureus (strain N315)
(Species: Staphylococcus aureus
(Species: Staphylococcus aureus
(Species: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
(State: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
(State: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-oct-2001
(State: Till to the plant of the 
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A;Experimental source: strain N315
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 28;
1; Mismatches
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Pred. No. 11;
1; Mismatches
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A, Residues: 1-260 <arn>
A, Cross-references: GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD05628.1; PID:g415455
A, Experimental source: strain J99
C, Genetics:
A; Gene: jhp0046
                                                                                                                                                                            0;
                                                                                                                                                                         0; Gaps
                                                                                                                           Query Match
52.6%; Score 40; DB 2; Length 260;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels
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Search completed: October 14, 2003, 08:40:48 Job time: 10.3864 secs

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GenCore version 5.1.6
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October 14, 2003, 08:35:36; Search time 4.13636 Seconds (without alignments) 147.798 Million cell updates/sec Run on:

US-09-931-700-2 76 1 YGGHQIYQFTDKD 13 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_41:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | scr            | P35318 homo sanien | rattu    | P53366 sus serofa | pos        | cani       |            |           | 026346 methanobact | P27028 flavobacter | P51862 saccharomyc |            | P28582 daucus caro |            |           |            |            | Ē  |            |            |            | 083047 treponema p |            |                  | Sa         |            |            | P96086 thermoplasm |           |           | 33         | 10         | 140        |            |
|-----------|----------------|--------------------|----------|-------------------|------------|------------|------------|-----------|--------------------|--------------------|--------------------|------------|--------------------|------------|-----------|------------|------------|--|------------|------------|------------|--------------------|------------|------------------|------------|------------|------------|--------------------|-----------|-----------|------------|------------|------------|------------|
| SUMMARIES | ID             | ADM                | ADML_RAT | ADML_PIG          | ADML_BOVIN | ADML_CANFA | ADML_MOUSE | SYN_DROME | SYH_METTH          | PPCE_FLAME         | ROM2_YEAST         | TKSU_PYRKO | CDPK_DAUCA         | DEXT_STRDO | AMY_STRVL | HIS6_VIBCH | SI7D_HUMAN | SI7D_MOUSE                                       | Y205_MYCTU | CBPT_THEVU | SAHH_CAUCR | DNAA_TREPA         | SNXI_HUMAN | ETFD_SCHPO       | YNL5_YEAST | GRIA_BACCE | X379_HUMAN | - 1                | AMY_STRGR | AMY_STRLM | VATF_DESSY | YKFG_ECOLI | YFJY_ECOLI | UL31_HSV11 |
|           | DB             | Н                  | Н        | Н                 | Н          | Н          | Н          | Н         | <b>-</b>           | н.                 | Н                  | Н.         | Н                  | Н.         | -         | Н          | <b>⊢</b>   | <del>,                                    </del> | Н          |            | П          | Ţ                  | П          | <del>, -</del> 1 | Н          | Н          | Н          | Н                  | Н         | Н         | H          | Н          | Н          | 7          |
|           | Length         |                    | 185      | 188               | 188        | 188        | 1.84       | 980       | 425                | 705                | 1356               | 422        | 532                | 1337       | 569       | 257        | 302        | 360  | 367        | 424        | 463        | 464                | 628        | 632              | 644        | 663        | 1059       | 1071               | 266       | 266       | 102        | 158        | 160        | 306        |
| deр       | Query<br>Match | Ŋ                  | 2        | S                 | 8          | 68.4       | ^          | 9         | м,                 | ⊣.                 | - 1                | $\circ$    | $\circ$            | 0          | on .      | ന          | œ ·        | ∞ .  | 8          | œ          | α          | 48.7               | φ.         | 48.7             | 48.7       | 48.7       | 48.7       | 48.7               | 48.0      | 48.0      | 47.4       | 47.4       | 47.4       | 47.4       |
|           | Score          | 57                 | 57       | 57                | 52         | 52         | ω,         | 5.5       | 2. C               | n (                | 50 C               | 800        | 89                 | ~          | 37.5      | 37         | 37         | 37   | 37         | 37         | 37         | 37                 | 3.7        | 3.7              | 3.7        | 37         | 37         | n                  | 36.5      |           | 36         |            |            |            |
|           | Result<br>No.  | н                  | 64       | m                 | 4          | in i       | וט         | ~ (       | 200                |                    | T 7                | 7.         | 77                 | FT -       | 7.<br>7.  | 15         |            | / [  | 30 G       | 19         | 20         | 21                 | 22         | 57               | 47         | 25         | 7 2 6      | 17                 | 58        | 67        | 30         | 31         | 3.5        | 33         |

| Q8cze6 oceanobacil<br>P46831 mycobacterii<br>Q8z2q2 s qlucosami<br>Q93831 candida alb<br>Q27421 drosophila<br>P4735 mycoplasma<br>Q40519 nlcotiana t<br>Q40070 hordeum vul<br>P10690 spinacia ol<br>P25210 petromycon<br>P39594 bacillus su<br>Q97vp5 sulfolobus   |
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# ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is a so long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC COMPROS. OF FULLD AND ELECTROLYTE HOMEOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP INHIBIT ALDOSTERONE SECRETION BY DIRECT ARRENAL ACTIONS. IN FIGURARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN ACHIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD.
                                                                                                                                                                                                                                                                                                  MEDLINE=20053666; PubMed=10588445;
Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
"Structure-activity relationships of adrenomedullin in the circulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (G-42 PROVIDE AMIDE GROUP).
                                                          Matsuo H., Eto T.; "Adrenomedullin: a novel hypotensive peptide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hormone; Amidation; Cleavage on pair of basic residues; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTC
ADERNAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                          Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PREPROAM C-TERMINAL FRAGMENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G0:0006171; P:cAMP biosynthesis; TAS.
G0:0007267; P:cell-cell signaling; TAS.
G0:00080155; P:pregnancy; TAS.
G0:0006701; P:pregnancy; TAS.
G0:0006701; P:progesterone biosynthesis; TAS.
G0:0006711; P:response to wounding; TAS.
G0:0007165; P:signal transduction; TAS.
                                                                                                                 Biochem. Biophys. Res. Commun. 192:553-560(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0005615; C:extracellular space; TAS. GO:0005625; C:soluble fraction; TAS.
                                                                                                                                                                                                                  "Proadrenomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMIDATION
AMIDATION
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Pfam; PF02039; Adrenomedullin; 1.
IISSUE=Pheochromocytoma;
MEDLINE=93249425; PubMed=8387282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S73906; AAC60642.1; --
BC015961; AAH15961.1; --
D43639; BAA07756.1; ALT_SEQ.
                                                                                                                                                                              MEDLINE=98240137; PubMed=9578982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00801; ADRENOMEDULN.
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                                                                                                                                                                                                                                                                                                                                                                                        85:1-8(1999).
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41
92
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Genew; HGNC:259; ADM.
                                                                                                                                                                                                                                                                                                                                                              and adrenal gland.";
Regul. Pept. 85:1-8(
                                                                                                    pheochromocytoma.";
                                                                                                                                                                                                   Samson W.K.;
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MOD_RES
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PROPEP
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Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
"Discovery of adrenomedullin in rat ischemic cortex and evidence for
its role in exacerbating focal brain ischemic damage.";
Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
-- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuo H., Eto T.; "Molecular cloning and biological activities of rat adrenomedullin, a
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
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                                                                                               75.0%; Score 57; DB 1; Length 185; 100.0%; Pred. No. 0.0068; Pred. No. 0.1068; Ive 0; Mismatches 0; Indels
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PREPROAM C-TERMINAL FRAGMENT
                                               20420 MW; 64C7D2AOB4654DFE CRC64;
R (in dbSNP:5005).
1=VAR_014861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypotensive peptide.";
Blochem. Blophys. Res. Commun. 195:921-927(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley; TISSUE-Adrenal gland; MEDLINE-93384621; PubMed-7690563;
                                                                                                                                                                                                                                                                                                                                                                                                   185 AA
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InterPro; IPR001710; Adrenomedullin.
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PRINTS; PR00801; ADRENOMEDULN.
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EMBL; U15419; AAB60519.1; -.
                                                                                                                        Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                       122 HQIYQFTDKD 131
                                                                                                                                                                                                          4 HQIYQFTDKD 13
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91
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185
                                            185 AA;
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P43145;
                                            SEQUENCE
                                                                                                  Query Match
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-i- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.; "Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding its precursor."; FEBS Lett. 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
          AMIDATION (G-42 PROVIDE AMIDE GROUP) (BY SIMILARITY).
AMIDATION (G-144 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00801; ADRENOMEDULN.
Hormone; Amidation; Cleavage on pair of basic residues; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y., Kawamoto M., Minamino N., Matsuo H., Eto T.; "Identification and hypotensive activity of proadrenomedullin N-terminal 20 peptide (PAMP)"; FEBS Lett. 351:35-37(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULLIN.
PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                Score 57; DB 1; Length 185;
Pred. No. 0.0068;
Mismatches 0; Indels
                                                           35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                           SIMILARITY)
                                                                                                                                                                                                                      188 AA.
                                                                                                          0; Mismatches.
SIMILARITY
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InterPro; IPRO01710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                   75.0%; Score
                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 22-41.
TISSUE-Adrenal medulla;
MEDLINE-94357274; PubMed-8076689;
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94139945; PubMed-8043068;
                                                (BY
                                                           185 AA; 20636 MW;
                                                                                              100.08;
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                                                                                                          10; Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                               rissum-Adrenal medulla;
                                                                                                                                  4 HQIYQFIDKD 13
                                   143
                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9823;
           41
                                   143
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PROPEP
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PROPEP
DISULFID
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                                   MOD_RES
           MOD_RES
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between the Swiss Institute of Bloinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98244567; PubMed=9585168;
Barker S., Wood E., Clark A.J.L., Corder R.;
"Cloning of bovine preproadrenomedullin and inhibition of its basal expression in vascular endothelial cells by staurosporine.";
Life Sci. 62:1407-1415(1998).
-i- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
                                       AMIDATION (G-42 PROVIDE AMIDE GROUP).
AMIDATION (G-147 PROVIDE AMIDE GROUP).
71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMIDATION (G-147 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Boyidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 \\ 21 \\ \mathrm{BY} SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 52; DB 1; Length 188;
Pred. No. 0.052;
                                                                                                                                 Length 188;
                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIRCULATION CONTROL (BY SIMILARITY).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                              Score 57; DB 1; 1
Pred. No. 0.0069;
                                                                                                                                                                                                                                                                                                                                                                                   188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                           0; Mismatches
SIMILARITY).
BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001710; Adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ001613; CAA04866.1; -
                                                                                      20893 MW;
                                                                                                                            75.0%; ;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20981 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.4%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                              Query Match 75.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                    122 HQIYQFIDKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92
146
188
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                                                             146
                                                                                                                                                                                                                        4 HQIYQFTDKD 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus (Bovine).
                  110 1
41
146 1
188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Aorta;
                                                                                                                                                                                                                                                                                                                                                                                ADML_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                          MOD_RES
MOD_RES
SEQUENCE
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                     DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
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PEPTIDE
PROPEP
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    RESULT 6
                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                            ono Y., Kojima M., Okada K., Kangawa K.;
"cDNA cloning of canine adrenomedullin and its gene expression in the heart and blood vessels in endotoxin shock.";
shock 10:243-247(1998).
-1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
PEPTIDE 22 41 PROADRENOMEDULLIN N-20 IERMINAL PEPTIDE.
                                                                                                      16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BI SIMILIANI).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMIDATION (G-42 PROVIDE AMIDE GROUP) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                               Imoto I., Jougasaki M.;
"Cloning of cDNA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  809D6A64F98F5578 CRC64;
                                                                                                                                                                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 1;
Pred. No. 0.052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
ADRENOMEDULLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U96127; AAD09957.1; -.
INTERPO, IPRO01710; Adrenomedullin.
Pram; PF02039; Adrenomedullin; 1.
PRINTS; PR00601; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                     MEDLINE=99002704; PubMed=9788655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                   077559; Q9TVC9;
16-0CT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF045773; AAD05423.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.06;
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                                                                          STANDARD;
                     122 HQIYHFTDKD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||||||
HQIYQFTDND 131
4 HQIYQFTDKD 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 HQIYQFTDKD 13
                                                                                                                                                               Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=9615;
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45
95
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                                                                                                                                                                                                                                                                                                                                                    AGENTS.
                                                                          ADML_CANFA
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PROPEP
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                                                              ADML_CANFA
                                                     RESULT 5
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                                                                                                                                         Proadrenomedullin N-20
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                    16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-SCT-2001 (Rel. 40, Last sequence update)
16-SEP-2003 (Rel. 42, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-2(terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Expression of adrenomedullin, a hypotensive peptide, in the trophoblast giant cells at the embryo implantation site in mouse."; Dev. Biol. 203:264-275(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BI SIMILARIII).
AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; Genomic organization, expression, and chromosomal mapping of the mouse adrenomedullin gene"; Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARÍTY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL
1
21
BY SIMILARITY.
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0
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Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 1; Length 184;
Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF. 2).
C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
     184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97092892; PubMed=8938454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
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90.08;
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Best Local Similarity 90.v.,
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 HOLYOLTDKD 129
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:108058; Adm.
                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KO M.S.H.;
ADML_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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SYH_METTH
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                    DATE OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS SYN-S AND SYN1-RT).
STRAIN=Berlin; TISSUB=Head;
MEDLINE=96209149; PubMed=8627354;
Klagges B.R.E., Heimbeck G., Godenschwege T.A., Hofbauer A.,
Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Invertebrate synapsins: a single gene codes for several isoforms in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOId=024546-2; Sequence=VSP_006324;
-1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM.
-1- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform Syn-S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              980 AA; 102799 MW; E6037AZA4804F944 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          006324
                                                                               024546; Q24545;
30-MAY-2000 (Rel. 39, Created)
26-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.9%; Score 45.5; 52.6%; Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId-Q24546-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001359; Synapsin.
Pram; PF02078; Synapsin.
Pram; PF02150; Synapsin.C. 1.
PRINTS; PR01368; SYNAPSIN.
PROSITE; PS00415; SYNAPSIN.J: FALSE_NEG.
PROSITE; PS00416; SYNAPSIN.Z; FALSE_NEG.
Synapse; Neurone; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER. POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 YGGVPSINSLHSIYQFQDK 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, X95453; CAA64722.1; -.
HSSP; P17599; 1AUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0004575; Syn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 52.69
                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name-Syn1-RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Syn-S;
                                                                                                                                                                                            SYN OR SYN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buchner E.;
                                                                 SYN_DROME
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                                                                                                                                                                          Synapsin.
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DOMAIN
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               RESULT 7
SYN_DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Addredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; C. T. Caratyric Activity: ATP + L-histidine + tRNA(His) - AMP + Giphosphate + L-histidil-tRNA(His).

C. I. SUBCELJULAR LOCATION: Cytoplasmic.
C. I. SUBCELJULAR LOCATION: Cytoplasmic.
C. I. SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Prolyl endopeptidase precursor (EC 3.4.21.26) (Proline-specific endopeptidase) (PSE) (Post-proline cleaving enzyme) (PE).
                                                        15-JUL-1998 (Rel. 36, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.3%; Score 39; DB 1; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425 AA; 48019 MW; 8388A5975A017535 CRC64;
425 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                        Methanobacteriaceae; Methanothermobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HANDE, ME_00127; -; 1.
InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004154; Hiss.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR006195; tRNA_ligase_II.
Pfam; PF03129; HGTP_anticodon; 1.
Pfam; PF00587; tRNA_synt_2b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000811; AAB84750.1; ALT_INIT.
HSSP; 032422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 77.8 tes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 HQIYQFTDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 NQIYHFTDK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 425 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Delta H;
                                                                                                                                                                                                                                  HISS OR MTH244.
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P27028;
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PRT; 1356 AA

STANDARD;

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ROM2_YEAST
P51862;
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                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=92176159; PubMed=1840588;
Yoshimoto T., Kanatani A., Shimoda T., Inaoka T., Kokubo T., Tsuru D.;
"Prolyl endopeptidase from Flavobacterium meningosepticum: cloning and sequencing of the enzyme gene.";
J. Blochem. 110:873-878(1991).
                                                                                                                                                                                                                                                     MEDLINE-94114173; PubMed-7764331;
Diefenthal T., Dargatz H., Witte V., Reipen G., Svendsen I.;
Cloning of proline-specific endopeptidase gene from Flavobacterium meningosepticum: expression in Escherichia coli and purification of the heterologous protein.,
Appl. Microbiol. Biotechnol., 40:90-97(1993).

1- FUNCTION: CLEAVES PEPTIDE BONDS ON THE C-TERMINAL SIDE OF PROLYL RESIDUES WITHIN PEPTIDES THAT ARE UP TO APPROXIMATELY 30 AMINO ACIDS LONG. HAS AN ABSOLUTE REQUIREMENT FOR AN X-PRO BOND IN THE TANKS CONFIGURATION IMMEDIATELY PRECEDING THE PRO-Y SCISSIBLE
               Flavobacterium meningosepticum (Chryseobacterium meningosepticum).
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Hydrolysis of Pro-|-xaa >> Ala-|-xaa in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC0EDCBABB328256 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRO01375; Peptidase_S9.
InterPro; IPRO04106; Peptidase_S9.N.
InterPro; IPRO04471; Prol_endopep_ser.
InterPro; IPR002470; Proligo_Prase.
InterPro; IPR00379; Ser_setrs_site.
Pfam; PF00326; Peptidase_S9; 1.
Pfam; PF00387; Peptidase_S9; 1.
Pfam; PF00387; Peptidase_S9, N.
Pfam; PF00389; Peptidase_SPR; 1.
Pfam; Pf00389; Pf00389; Pf00389989; Pf003891; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROLYL ENDOPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Periplasmic.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S -> C (IN REF. 2).
R -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 39;
1; Mismatches
                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39;
                                                      Flavobacteriaceae; Chryseobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10980; BAA01755.1; -. EMBL; X63674; CAA45213.1; -.
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Best Local Similarity 65...
7; Conservative
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705
556
675
110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligopeptides.
SUBUNIT: Monomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; JX0194; JX0194.
HSSP; P23687; 1QFM.
MEROPS; S09.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556
675
110
587
705 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
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SEQUENCE FROM N.A.

STRAIN-S2886 / AB972;
MEDLINE-97313267; PubMed-9169871;
A Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
Benes V., Brueckner M., Delius H., Bebling U., Hennann K.,
Benes V., Brueckner M., Delius H., Mebois E., Duesterhoeft A.,
Benes V., Brueckner M., Delius H., Milose T., Kleine K.,
Benes V., Brueckner W., Mewes H.-W., Miosga T., Moester P.,
Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
Mueller-Auer S., Nentwich U., Obermater B., Piravandi E., Pohl T.M.,
Rochaffe M., Scherens B., Scholler P., Schwarz S.,
Charfe M., Scherens B., Scholler P., Schwarz S.,
Charfe M., Scherens B., Scholler P., Schwarz S.,
Charfe M., Verhasselt P.,
Mederwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
Wedler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler H., Zimmermann F.K., Zollher A., Hani J., Höhelsel J.D.;
Medler M., Aller M., Weller B., Medler M., Weller B., Sollander A., Hani J., Höhelsel J.D.;
Medler M., Sollander M., Weller B., Sollander B., Solland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGD; SGO04363; ROWZ.

GO; GO:0005934; C:bud tip; IDA.

GO; GO:0005934; C:bud tip; IDA.

GO; GO:000589; F:Rho guanyl-nucleotide exchange factor activity; IDA.

GO; GO:00074871; F:Rho guanyl-nucleotide exchange factor activity; IDA.

GO; GO:0007117; P:bud growth; IPI.

GO; GO:00070283; P:establishment of cell polarity (sensu Sacch.

GO; GO:000283; P:establishment of cell polarity (sensu Sacch.

InterPro; IPRO01889; Citron.

InterPro; IPRO01391; GDS_CDC24.

InterPro; IPRO01311; GDS_CDC24.

InterPro; IPRO01319; RhoGEF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OZAKI K., Tanaka K., Imamura H., Hihara T., Kameyama T., Nonaka H., Hirano H., Matsuura Y., Takai Y.; Kameyama T., Nonaka H., Hirano H., Matsuura Y., Takai Y.; Rameyama T., Matsuura Y., Takai Y.; Rameya M. Rom2p are GDP/GIP exchange proteins (GBPs) for the Rholp Small GTP binding protein in Saccharomyces cerevisiae."; EMBO J. 15:2196-2207(1996).
                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                         Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
115-SEP-2003 (Rel. 42, Last annotation update)
ROM2 OF YER371W OR L8039.3.
                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00741; DH_1; FALSE_NEG. PROSITE; PS50010; DH_2; 1. Guanine-nucleotide releasing factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96208506; PubMed=8641285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U19103; AAB67564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00780; CNH; 1.
Pfam; PF00610; DEP; 1.
Pfam; PF00621; RhoGEF; 1.
SMART; SM00036; CNH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00325; RhoGEF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S51389; S51389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTP-BOUND FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION.
                                                                                                                                                                                                                                                                                    NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
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Gaps

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Indels

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ROM2\_YEAST RESULT 10

50 GGHIVYQF 57

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Transferase;
                                                                                                            01-DEC-1992
                                                                               CDPK_DAUCA
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                               CDPK_DAUCA
                                              RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kannan Y., Koga Y., Inoue Y., Haruki M., Takagi M., Imanaka T., Morikawa M., Kanaya S.;
Morikawa M., Kanaya S.;
"Active subtilisin-like protease from a hyperthermophilic archaeon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Secreted.
-1- MISCELLANEOUS: Thermostable; high activity at 80 degrees Celsius.
                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TK-SUBTILISIN.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a form with a putative prosequence.",
Appl. Environ. Microbiol. 67:2445-2452(2001).
-1- FUNCTION: Has a borad substrate specificity with a slight
preference to large hydrophobic amino acid residues at the Pl
                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00136; SUBTILASE_ASP; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
Hydrolase; Serine protease; Calcium-binding; Zymogen; Signal.
                                                              Score 39; DB 1; Length 1356;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 38; DB 1; Length 422; 75.0%; Pred. No. 34;
329 336 POLY-HIS.
632 635 POLY-ASP.
1356 AA; 152595 MW; 5FBC542114E7BC92 CRC64;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              843255BCD806DB71 CRC64;
                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimal pH is 9.5.
SIMILARITY: Belongs to peptidase family S8
                                                                                                                                                                                                                                              TKSU_PYRKO STANDARD; PRT; 422 AA. PSB507: 0977F5; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                Tk-subtilisin precursor (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000209; Peptidase_S8.
Pfam; PF00082; Peptidase_S8; 1.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21268834; PubMed=11375149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43785 MW;
                                                               51.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AB056701; BAB60701.1;
                                                                                                                                                                                                                                                                                                                                                   Pyrococcus kodakaraensis.
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              position.
COFACTOR: Calcium.
                                                                                                                                                    |::|:||
496 HEVYEFTD 503
                                                                                                                                 4 HQIYQFTD 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=69014;
                                                                                                                                                                                                                                                                                                                                                                                      Thermococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
ACT_SITE
                 DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                   TKSU_PYRKO
                                                                                                Matches
                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                               FT
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                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Apiales; Apiaceae; Daucus.
NCBL_TaxID=4039;
                                                                                                                                                                                                                                   SEQUENCE OF 108-532 FROM N.A. MEDINE-92008564; Pubmed-1912486; Suen K.-L., Choi J. H.; "Isolation and sequence analysis of a cDNA clone for a carrot "Isolation and sequence analysis of a cDNA clone for a carrot
                                                                                                                                                                                                                                                                                                                                                                                                                 CAMK SUBFAMILY.
SIMILARITY: Contains 4 EF-hand calcium-binding domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                         Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F03E6F036A0AE348 CRC64;
                           01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Calcium-dependent protein Kinase (EC 2.7.1.-) (CDPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
EF-HAND 3 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF-HAND 4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE
532 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE: PS00018; EF HAND: 4.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP, Q63450; 1A06.
InterPro; IPR002048; EF-hand.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR0002290; Ser_thr_pkinase.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00036; efhand; 4.
Pfam; PF00069; pkinase; 1.
Probom; PD000012; EF-hand; 2.
Probom; PD000011; Prot_kinase; 1.
SMART; SM00054; EFh; 4.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation.
                          24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X56599; CAA39936.1; -.
STANDARD;
                                                                                      Daucus carota (Carrot)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S17759; S17759.
PIR; T14335; T14335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500
532 AA;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA_BIND
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60065 MW;

SEQUENCE

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Gaps

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Indels

1;

1; Mismatches

Conservative

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Matches

2 GCHQIYQF 9

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                                    ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wanda S.-Y., Curtiss R. III:

"Purification and characterization of Streptococcus sobrinus
dextranase produced in recombinant Escherichia coli and sequence
analysis of the dextranase gene.";

J. Bacteriol. 176:3983-3850(1994).

-I-FUNCTION: MAY PLAY A SUCRE IN SUCROSE-INDEPENDENT ADHERENCE TO THE
PELLICLE-COATED TOOTH SURRACE.

-I-CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic
-I-SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
-!- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1308 1308 AMIDE-LINKED TO CELL WALL (POTENTIAL).
1337 AA; 143298 MW; B494275A77A2E3D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat; Signal; Plasmid.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEXTRANASE.
REMOVED BY SORTASE (POTENTIAL).
LPXTG SORTING SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.0%; Score 38; DB 1; Length 1337; 41.7%; Pred. No. 1.1e+02;
Score 38; DB 1; Length 532; Pred. No. 44;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-
                                                                                                                                                                                                                                                                                                                                            Streptococcus downei (Streptococcus sobrinus)
                                                                                                                                                                                                 PRT; 1337 AA.
                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
STRAIN=6715 / UAB66:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00746; Gram_pos_anchor; 1.
TIGRFAMS; TIGR01167; LPXTG_anchor; 1.
PROSITE; PS50847; GRAM_POS_ANCHORING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR006192; LPXTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94292401; PubMed=8021165;
                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequestrenesser-2003 (Rel. 42, Last annotation)
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M96978; AAA21772.1; -.
                                    6; Conservative
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1308
1337
1309
1308
                                                                                             || :|: |||
458 HQAFQYFDKD 467
                                                                      4 HQIYQFTDKD 13
                 Best Local Similarity
                                                                                                                                                                                                                                                                                                            .ucanohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1317;
                                                                                                                                                                                                                                                                                                                                                               Plasmid pYA902.
                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=6715
                                                                                                                                                                                             DEXT_STRDO
P39653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITE
                                    Matches
                                                                                                                                                             RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                       Virolle M.-J., Long C.M., Chang S., Bibb M.J.; "Cloning, characterisation and regulation of an alpha-amylase gene
                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Intrages in oligosaccharides and polysaccharides. -!- INDUCTION: BY MALTOSE, AND REPRESSION BY GLUCOSE. -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 569;
                                                                                                                                  Streptomyces violaceus (Streptomyces venezuelae),
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                 01-AUG-1991 (Rel. 19, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWART; SW00632; Aamy_C; 1.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

14CA5B1D56720043 CRC64;
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569 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA-AMYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; JS0101, JS0101.
HSSP, P2957; LAOM.
InterPro; IPR006589; Alp_amyl_cat_sub.
InterPro; IPR006648; Alpha_amyl_c.
InterPro; IPR006647; Alpha_amyl_cat.
InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR002044; CBD_4.
InterPro; IPR00124; Glyco_hydro_l3.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF00128; Alpha-amylase; 1.
Pfam; PF00686; CBM_20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49.3%; Score 37.5; 50.0%; Pred. No. 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=ATCC 15068;
MEDLINE=89232724; PubMed=3266752;
                                                                                                                                                                                                                                                                                                       from Streptomyces venezuelae.";
Gene 74:321-334(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0110; ALPHAANYLASE.
PRODOM; PD001569; CBD_4; 1.
SMART; SMO0642; Aamy; 1.
SMART; SMO0632; Aamy_C; 1.
                                01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60637 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 YGSPDVHSGYEWTDKD 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M25263; AAB36561.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YGG---HQIYQFTDKD 13
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
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                                                                                                       glucanohydrolase).
                                                                                                                                                                                     NCBI_TaxID-1936;
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 AMY_STRVL
P22998;
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ACT_SITE
SEQUENCE
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Gaps

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3; Indels

4; Mismatches

Conservative

Best Local Similarity Matches 5; Conserv

2 GGHQIYQFTDKD 13

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                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=El TOR Ni6961 / Serctype Ol;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase subunit hisF) (ImGP synthase subunit hisF) (IMGP synthase cyclase)
                                                                                                                                                                                                                                                                                                                                                                "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.7%; Score 37; DB 1; Length 257; 66.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 AA; 28338 MW; F722BBC43BEB153C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histidine blosynthesis; Lyase; Complete proteome.
          257 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR003009; FWN_enzyme.
InterPro; IPR006062; His_biosynth.
InterPro; IPR004651; HisF.
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00977; His_biosynth; 1.
TIGREAMS; TIGR00735; hisF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004193; AAF94297.1; -.
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              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; E82238; E82238.
TIGR; VC1138; -.
HAMAP; MF_01013; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                 Vibrio cholerae.
                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                             Fraser C.M.;
            HIS6_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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HIS6_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Job time : 7.13636 secs

Search completed: October 14, 2003, 08:39:09

GOYOVYOFT 146

138

2 GGHQIYQFT 10

QY Db Q913b4 pseudomonas Q8vte0 helicobacte Q8vtb6 helicobacte Q8vtb3 helicobacte Q8vt13 helicobacte Q8vt13 helicobacte Q8vte5 helicobacte Q8vte8 helicobacte Q8vte8 helicobacte Q8vte8 caenorhabdi

Q8kc18 chlorobium Q9bsu7 homo sapien Q991f0 mus musculu

Q8s011 oryza sativ Q943e0 oryza sativ Q8chg6 mus musculu

015031 homo sapien Q9usq7 schizosacch Q8epg1 oceanobacil

062214 caenorhabdi 099x71 staphylococ QBnyq7 staphylococ 076322 loligo peal 076323 loligo peal

Q9ugx0 homo sapien Q9i3b4 pseudomonas

Q9chs8 lactococcus

Q9sv96 arabidopsis Ogutt2 schizosacch Og1474 lactococcus

OM protein

Run on:

Searched:

Database

Sednence:

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MEDLINE-96157714; PubMed-8576091; MEDLINE-96157714; PubMed-8576091; MEDLINE-96157714; PubMed-8576091; Lohiki v., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.; Distribution and characterization of immunoreactive adrenomedullin in porcine tissue, and isolation of adrenomedullin [26-52] and adrenomedullin [34-52] from porcine duodenum."; J. Biochem. 118.765-770(1995). InterPro; IPR001710; Adrenomedullin.
PF02039; Adrenomedullin: 1.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 6; Length 27;
Pred. No. 0.0097;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B8DC7FA18D8B3D90 CRC64;
                                                                                                                                                                                                                                                                                                                                 27 AA.
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                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            095KPO;
01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                08VLL3
08VTE5
08VTE8
016622
0965L2
08KCL8
                091.474
09CHSB
062214
099X71
08NY07
                                                                                                       Q9ZN14
Q8VTB6
Q8VTE3
                                                                                                                                                                                                        Q8S011
Q943E0
Q8CHG6
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Q8VTE0
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                                                            076322
076323
Q9UGX0
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100.0%; Pre-
0; !
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16
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Best Local Similarity 100.
Matches 10; Conservative
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Sus scrofa (Pig).
44444422
24444444
114444
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                                                                                      SEQUENCE
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Q9TRZ6
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Q8inm4 drosophila
Q24544 drosophila
Q9vh15 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9x5r9 streptomyce
Q9zkk7 helicobacte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ewq4 streptomyce
Q45612 bacillus su
Q9a5r9 caulobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              081050 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8rcv8 thermoanaer
Q19582 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8mxj0 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8inm6 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9trz6 sus scrofa
Q95kp0 bos taurus
                                                       October 14, 2003, 08:36:06; search time 17.4318 Seconds (without alignments) 192.446 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                            830525
               Compugen Ltd.
      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compug
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                          830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q95KP0
Q55549
Q81NM4
Q24544
Q9VH15
Q81NM6
Q81NM6
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Q45612
Q9A5R9
Q8RCV8
Q19582
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Q8MXJ0
                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                     sp_unclassified:*
                                                                                                                                                                                                                                                                                    sp_fungi:*
sp_human:*
sp_invertebrate:*
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sp_phage:*
                                                                                                              1 YGGHQIYQFTDKD 13
                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                 sp_archea:*
sp_bacteria:*
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sp_rodent:*
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                                                                                             US-09-931-700-2
76
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Match Length
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173
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280
324
326
350
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45.5
45.5
45.5
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                                                                                                                                Scoring table:
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0;

Gaps

0;

Result No.

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
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                                                            Matches
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Q8INM4
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
Kangawa K., Eto T.;
"ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96127529; PubMed-8590279; Rotani H., Sazuka T., Miyajima N., Raneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S., Seto S., Kotani H., Sazuka S., Saguence analysis of the genome of the unicellular cyanobacterium "Sequence analysis of the genome of the unicellular ryanobacterium region from map positions 64% to 92% of the genome."; In the 1 Mb INA Res. 2:153-166(1995).
                                                                                                                      Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52; DB 6; Length 188; Pred. No. 0.54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055107; BAB62176.1; -. InterPro; IPR001710; Adrenomedullin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 3:109-136(1996).

EMBL. D63999, BAA10047.1; --
HYPOThetical protein; Complete proteome,
SEQUENCE 643 AA; 68369 MW; 1EE9001D3332B411 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20963 MW; 6102E69A756DCA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID=1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein slr0168.
   (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-97061201; PubMed-8905231;
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90.0%;
   01-DEC-2001 (TremBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 HQIYQFTDKD 13
                                                                                                                                                                                                            Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=PCC 6803;
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                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                            Adrenomedullin.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Fashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Burdon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,
RA Barladon R.C., Baxter E.G., Helt G., Nolson C.R., Gabor G.L.
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Barlaw R.M., Basu A., Baxendale J., Bayraktaroquel L., Beasley E.M.,
Besson K.Y., Bencos P.V., Berman B.P., Bhandari D., Holshakov S.,
Burtis R.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Bayenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Perriaer S., Pleits Chman M.,
RA Cherry J.M., Capler A., Dan R.A., Garger R., Gargel C., Gabriellan A.E., Garg W. D., Galbart W.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Garz, Gelbart W.M., Glasser K.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Harris M.L.
Alasko P., Lei Y., Levitsky R.A., Li J., Mill M. H., Ibeywam C.,
Alasko P., Lei Y., Levitsky R.A., Li J., Mill J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Musher D.M., Nelson D.L.,
Ra Razzollo M., Pittman G.S., Pan S., Pollard J., Purl V., Receb M.G.,
Randert K., Moy M., Murphy B., Murphy L., Musher M., Sanith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong S., Yao Q.A., Ye J.,
Ra Jenert K., Moy M., Wanshoon M., Strong S., Yao Q.A., Ye J.,
Whilams S.M., Woodager, Worley K.C., Wu D., Yang S., Ran H.,
Spier E., Spradling A.C., Stapleton M., Stung S., Ran B.,
Welson E.C., Shong F.N., Weinstock G.W., Weissenbach J.,
Raiber R., Moyel M., Weissenbach J.,
Raiber R., Moyer W., Weinstock G.W., Weiss
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                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Héxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Score 51; DB 16; Length 643; Pred. No. 3;
                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 AA
                                                                                        2; Mismatches
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                                                                                    8; Conservative
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                                                                                                                                                                    3 GHQIYQFTDKD 13
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01-MAR-2003
CG3985-PD.
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01-MAR-2003
       Query Match
Best Local 9
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                                         Matches
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MEDLINE=96209149; PubMed-8627354;
Klagges B.R., Heimbeck G., Godenschwege T.A., Hofbauer A.,
Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
                                                                                                                                                                             Mista S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kroumiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; "Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Invertebrate synapsins: a single gene codes for several isoforms in
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003686; AAN13464.1; "SEQUENCE 348 AA; 38321 MW; BFA837EF9A438134 CRC64;
                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      388 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.9%; Score 45.5; I
52.6%; Pred. No. 13;
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SYN OR SYN2 OR CG3985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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J. Neurosci. 16:3154-3165(1996).
EMBL; X95454; CAA64724.1; -.
HSSP; P17599; 1AUX.
FlyBase; FBgn0004575; Syn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 YGGVPSINSLHSIYQFQDK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001359; Synapsin.
Pfam; PF02079; Synapsin; 1.
Pfam; PF02750; Synapsin_C; 1.
PRINTS; PR01368; SYNAPSIN_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                SEQUENCE FROM N.A.
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Best Local Simi
Matches 10;
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburnen M., Henderson S.N.,
RA Gotyer R.A., Lewis S.E., Richards S., Ashburnen M., Pfediffer B.D.,
RA Button G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Randon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfediffer B.D.,
RA Ballow R.M., Bazu A., An H.J., Andrews-Péannkoch C., Baldwin D.,
RA Besson K.Y., Bennes P.V., Berman B.P., Bhandari D., Bolshakov S.,
Rokova D., Botchan M.R., Boutler H., Caddeu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
RA Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
RA Goton K., Doup L.E., Downes M., Diqan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis R.L., Harvey D., Hediman T.J., Hearnadez J.R., Houston W.A.,
RA Hostin D., Houston K.A., Howland T.J., Weil M.H., Ibegwam C.,
A Jabli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Anostin D., Houston K.A., Howland T.J., Weil M.H., Ibegwam C.,
Allali M., Mattel B., Wolfinesh T.G., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Melson D.R., Moy M., Murphy B., Murphy I., Marny D.M., Nelson D.L.,
Relanct K., Remington K., Sauders R., Paul B., Sant H.,
Rander K., Remington K., Sauders R., Shue B.C., Siden E., Shen H.,
Spier E., Spradling A.C., Simpelcon M., Stuons R., Shue B.C., Siden K., Wenssenbach J.,
Rulliams S.M., Woodserfy Worler E., Wang A.H., Wenssenbach J.,
Rulliams S.M., Woodserfy Worler S., Wang A.H., Wenssenbach J.,
Rulliams S.M., Woodserfy Worler S., Rome S.,
Rulliams S.M., Woodserfy Worler S., Rome S.,
Rulliams S.M., Woodserfy Worler S., Rome S.,
Rulliams 
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Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodsson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
                                                  7;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
       DB 5; Length 388;
                                                    Indels
                                                                                                                                                                                                                                                                                                (TrEMBLrel. 13, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                  5
                                                                                                                                                                                                                                                          443 AA.
  ; Score 45.5; DE
; Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20196006; Pubmed=10731132;
                                                                                          1 YGG-----HQIYQFTDK 12
                                                                                                                                     81 YGGVPSINSLHSIYQFQDK 99
59.9%;
                                               10; Conservative
                          Similarity
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MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
A Manatides P.G., Scherer S.E., Tip P.W., Hoskins R.A., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Bril J.R., Agbayani A., An H.J., Andrews-Ffannkor C.R., Gabor G.L.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Ballew R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Doubin K.J., Evangelista C.C., Ferriacra S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                         Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield E., Ansburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pardea V., Park S., Patel S., Piteiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Ventler J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome. "Sequencing of Drosophila melanogaster genome."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                    Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 45.5; DB 5; Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003686; ARF54506.2; -.
Flymase; PRO0004657; Syn.
SEQUENCE 443 AA: 47645 MW; DIB10DA3E655C59D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
CG3985-PB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YGG-----HQIYQFTDK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.9%;
52.6%;
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Best Local Similarity 52.64
Matches 10; Conservative
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A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A Hostin D., Houston K.A., Howland T.J., Wel M.H., Ibegyam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
A Jasko P., Lei Y., Lei Y., Lei Y., Kingly D., Lai Z.,
Liang Y., Lei Y., Lei Y., Lei Y., Lei Y., Liang Y., Lin X.,
A Lasko P., Lei Y., Lei Y., Lei Y., Liang Y., Lin X.,
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
A She B.C., Siden Kiamos I., Simpson M., Skrupski M.F., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Rhang Z.Y., Wassarman D.A., Weinstock G.W., Weissenbach J.,
A Hen R.F., Zaveri J.S., Zhan M., Zhou K., Zhu S., Zhu X., Smith H.O.,
A Lei Y., Myers E.W., Rubin G.M., Venter J.C.;
A The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celliker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

Bursc C.A., Gocayne J.D., Amenatides P.G., Brandon R.C., Rogers Y.,

Burscn J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

Rerijera S., Frise E., Galle R.F., Hostin D., Howland T.J.,

A Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

A Diegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,

McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

Phousenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

Stapleton M., Strong R., Svirskas R., Tactor C., Tyler D.,

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

Sequencing of Prosophila melanogaster genome.";
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Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hranger Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Bernan B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.; Annotation of Drosophila melanogaster genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.9%; Score 45.5; DB 5; Length 537;
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537 AA; 57691 MW; 782BE20B4BE60220 CRC64;
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0; Mismatches
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1 YGGHQIYQFTDKD 13
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8; Conservative
                                                                                                                                                                                             PRELIMINARY;
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                                                                                 66 GGHGIYQFYD 75
                                        2 GGHQIYQFTD 11
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Matches
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STRAIN=20083487; PubMed=10617197;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAen S.E., Ummayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Tsquence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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STRAIN-NRRL 2564;
MEDLINE-9201491; Pubmed=10099135;
MAO Y., Varoglu M., Sherman D.H.;
"Molecular characterization and analysis of the biosynthetic gene cluster for the antitumor antibiotic mitomycin C from Streptomyces lavendulae NRRL 2564.";
Chem. Biol. 6.251-263(1999).
EMBL; AF127374; AAD32724.1; -.
SEQUENCE 514 AA; 55697 MW; 888C7E685B8B2F2F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005313; AAC34478.1;
Interpro; IPR004342; EXS_Cterm.
Interpro; IPR004313; SPX.
Pfam; PF03124; EXS; 1.
Pfam; PF03124; EXS; 1.
Pfam; PF03105; SPX; 1.
SEQUENCE 776 AA: 89775 MW; BE30603ACFADD14E CRC64;
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Last annotation update)
                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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Pred. No.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GGHQIYQFTDKD 13
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STRAIN=cv. Columbia;
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Best Local Similarity
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                                                                                   At2g03240 protein.
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                                                                                                                                                                                          eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                         AT2G03240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., delonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Iyes C.,
Tummino P.J., Caruso A., Tieng O., Taylor D.E., Vovis G.F.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genomic sequence comparison of two unrelated isolates of the human
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Pred. No. 1.7e+02;
2; Mismatches 4; Indels (
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein C0869.1.
                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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PRT; 2231 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
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MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacteraceae; Helicobacter.
NCBI_TaxID=85963;
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STRAIN=168;
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"A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAIN-A3(2) / M145;
STRAIN-Balton Pubmed-12000953;
MEDLINE-21996410; Pubmed-12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Croin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Ollver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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SCO7673 OR SC4C2.08.
Streptomyces coelicolor.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 5; Length 173; Pred. No. 25;
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                                                                                         STRAIN-Bristol N2;
Geisel C., Stellyes L.;
"The sequence of C. elegans cosmid C08G9.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Materston R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036687; AAM75374.1; -.
WormPep; C0869.1; CE31155.
Hypothetical protein.
SEQUENCE 173 AA; 20056 MW; 2757D83377864CEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.3%;
58.3%;
Science 282:2012-2018(1998)
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Matches 7; Conservative
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                                                             SEQUENCE FROM N.A.
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Zhang J., Aronson A.I.;
"A Bacillus subtilis bglA gene encoding phospho-beta-glucosidase is
inducible and closely linked to a NADH dehydrogenase-encoding gene.";
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                                                                                                                                                                                                                                                                      Gaps
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"Cloning and sequencing of a 36-kb region of the Bacillus subtilis
genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995).
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"Isolation and characterization of a hydrogen peroxide resistant
mutant of Bacillus subtliss";
Microbiology 140:297-304(1994).
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                                                                                                                                                                                                     55.3%; Score 42; DB 16; Length 184; 54.5%; Pred. No. 26;
                                                                                                                                                                                                                                                                3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ogasawara N., Nakai S., Yoshikawa H.;
"Systematic sequencing of the 180 kilobase region of the
subtilis chromosome containing the replication origin.";
DNA Res. 1:1-14(1994).
                                                                                                                                                9E532A2748AFDE4A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                2; Mismatches
Nature 417:141-147(2002).

EMBL, AL939132; CAC17490.1; -.
InterPro; IPR005297; Lipoprotein_15.
Pram, PF03640; Lipoprotein_15; 2.
Lipoprotein; Complete protecome.
SEQUENCE 184 AA; 19107 MW; 9E532P
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Bacteriol. 176:1234-1241(1994).
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                                                                                                                                                                                                                                                                6; Conservative
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Search completed: October 14, 2003, 08:40:16
 Caulobacter crescentus.
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 A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Brington J., Fabret C., Ferrari E., Foulger D.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Denizot F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Denizot F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Halech J., Grandi G.,

RA Hibert H., Holsappel S., Hosono S., Hallo M.F., Itaya M., Jones L.,

A Choris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,

RA Noone D., O'Reilly M., Ogawa R., Ogiwara A., Oddega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sator T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sator M., Manbutk R., Wedler H., Weitzenegger T.,

RA Takeuchi M., Tamakoshi A., Taramanoto H., Yanane K., Yasamotot K., Yata K.,

RA Varia A., Wambutk R., Wedler E., Wedler H., Weitzenegger T.,

RA Varia A., Wambutk R., Wedler E., Wedler H., Waniers P., Robida K., Yasamotot H., Yanane K., Yasamotot K., Yata K.,

RA The complete genome sequence of the gram-positive bacterium Bacillus

Ra Princh P., Riber R., Radier R.,
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        Gardan R., Rapoport G., Debarbouille M.;
"Expression of the rocDEF operon involved in arginine catabolism in
Bacillus subtilis.";
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: D78193; BAA11297.1; -.
EMBL: Z99124; CAB16075.1; -.
                                                                                                                                Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
NAD-dependent epimerase/dehydratase family protein.
CC2378.
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MEDLINE=98044033; PubMed=9384377;
MEDLINE=95311309; PubMed=7540694;
                                                                 Mol. Biol. 249:843-856(1995).
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                                                                                                                  STRAIN=168;
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SEQUENCE FROM N.A.
MEDLINB-21173698, CD15;
MEDLINB-21173698, PubMed-11259647;
MEDLINB-21173698, PubMed-11259647;
MISTRIAN W., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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STRAIN=MB4 / JCM 11007;

MEDLINE-21992816; PubMed=11997336;

Bao O., Tian Y. Li W. Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;

Tan H., Chen R., Wang J., Yu J., Yang H.;

A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL; AR013002; AAM23593.1;
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBL_TaxID=155892;
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Pred. No. 49;
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Thermoanaerobacteriaceae; Thermoanaerobacter
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TIGRFAMs; TIGR00545; lipoyltrans; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001509; Epimerase_Dh.
Pfam; PF01370; Epimerase; 1.
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01-JUN-2002 (TrEMBLEEL 21,
01-OCT-2002 (TrEMBLEEL 22,
Lipoate-protein ligase A.
LPLA OR TIE0297.
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Matches 6; Conserv
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Job time : 21.4318 secs

Page 8

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(without alignments)
94.378 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
| SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                      163
1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                    OM protein
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                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           |   |        | Description     |   | Himan preproadreno |   | dad utttmennemerativ | Human adrenomedull | Human adrenomedil | יים מתובתחוד מתובתחוד | Adrenomedulin pep | Himan adrenomedul | The state of the s | Hallan agrenomedutt | Glycine extended h |          | GLYCine extended a |
|-----------|---|--------|-----------------|---|--------------------|---|----------------------|--------------------|-------------------|-----------------------|-------------------|-------------------|--|---------------------|--------------------|----------|--------------------|
| SUMMARIES |   |        | ID              | 14                                      | AAW25160           | 0 1 7 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F 2 F | 70 (1000)            | AAE09827           | AAB75110          | 0110044               | AABST / 38        | AAE09818          | ARD55104   | 10100               | AAB75111           | C1127GKK | ZTTC/GWW           |
|           |   |        | ЭВ              | 1                                       | 18                 | 22  | 1                    | 22                 | 22                | וכ                    | 77                | 22                | 7.7  | •                   | 22                 | 22       | 1                  |
|           |   |        | Match Length DB | t t 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | 31                 | 31  | 1                    | 31                 | 52                | L C                   | 70                | 52                | 52   | 1                   | 53                 | r,       | י                  |
|           | æ | Query  | Match           | 1 | 100.0              | 100 0                                       |                      | 100.0              | 100.0             | 100                   | 0.00              | 100.0             | 100.0  |                     | 100.0              | 00.0     |                    |
|           |   |        | Score           |   | 163                | 163   |                      | 163                | 163               | 163                   | 107               | 163               | 163  | 1 1                 | 163                | 163      | 1                  |
|           |   | Result | NO.             |   | -                  | 2   | 1 (                  | m                  | 4                 | ď                     | יי                | ø                 | 7  |                     | <b>3</b> 0         | σ        | ١                  |

| α~~ ~                                      | Universal stress p<br>Thioredoxin-(GSGSG<br>Human adrenomedull<br>Human adrenomedull<br>Adrenomedullin, in<br>Universal stress p | L L L L L L L L L L L L L L L L L L L                                | Mouse ischaemic co<br>Adrenomedullin pep<br>Adrenomedullin pep<br>Adrenomedullin pep<br>Human preproadreno<br>Novel human diagno<br>Novel human diagno<br>Novel human diagno | NOJIDJOSE PINOSPIOT<br>NOVEL human diagno<br>NOVEL human diagno<br>Bifidobacterium lo<br>Hypotensive peptid<br>Drosophila melanog<br>Novel human diagno<br>Clas I S-locus gly<br>Clas I S-receptor |
|--|--|--|--|--|
| 122  | ABJ186/1<br>AAB75114<br>AAB49697<br>AAB60344<br>ABP72347<br>ABJ18668   | AAB49698<br>AAB60345<br>AAB91768<br>AAE09819<br>AAB49699<br>AAB60346 | ABB5 / Z/09 AAB91767 AAB91765 AAW25159 ABG05415 ABG13273 ABG13273 AAWG09129  | AAWS6302<br>ABG11413<br>ABG10411<br>ABF67124<br>AAB67024<br>ABG1964<br>AAWS6306<br>AAWS6306  |
| 40000000                                   | 22224  | 222222   | 20000000000000000000000000000000000000   | 000000000000000000000000000000000000000  |
| 00000004                                   | 14/<br>170<br>185<br>185<br>206  | യ യ <b>4</b> സ യ യ യ   | 1-155 H D B B D  | 939<br>939<br>10<br>10<br>1096<br>436<br>846   |
| 1000.0<br>1000.0<br>1000.0<br>1000.0       |  |  |  | 301.3<br>301.3<br>301.3<br>301.3<br>300.7  |
| 888888888<br>90000000000000000000000000000 | 163<br>163<br>163<br>163   | 157<br>154<br>148<br>148<br>148                                      | 136.5<br>125.5<br>123.5<br>52<br>52<br>52<br>52<br>52  | 51<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10   |
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### ALIGNMENTS

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Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone; skin; blood related; disease; type II diabetes; preeclampsia; neurotransmission regulation; allergy; mast cell degranulation; antibacterial; antifungal; wound repair.
                                                                                                                                                                                                         /note= "residues 116-146 of preproadrenomedullin"
                                                                                   Human preproadrenomedullin derived immunogen, PO72.
                                                                                                                                                                                      Location/Qualifiers
                     AAW25160 standard; peptide; 31 AA.
                                                                                                                                                                                                                                 /note= "amidated"
                                                                                                                                                                                                                                                                                                                     96US-0013172.
95US-0002514.
95US-0002936.
                                                                                                                                                                                                                                                                                                  96WO-US13286.
                                                                 (first entry)
                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                    WO9707214-A1.
                                                                                                                                                                                                                                                                                                16-AUG-1996;
                                                                08-DEC-1997
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                18-AUG-1995;
30-AUG-1995;
                                                                                                                                                                                                                                                                          27-FEB-1997
                                                                                                                                                                                                                                                                                                                      12-MAR-1996;
                                          AAW25160;
                                                                                                                                                                                               Peptide
RESULT 1
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us-09-931-700-3.rag

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peptide receptor activity -
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             WPI; 2001-112059/12.
                                                                                                                                                                                                                                                                                                                                                                        31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6268474-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adrenomedullin (AM) peptides P070, P071, P072 and PAMP-20
were used for the production of anti-AM antibodies (Ab). P070 represents
preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
the N-terminus, P071 represents preproAM aa 122-131 with the sequence
Tyr-Gly-Gly attached at the N-terminus, P072 represents preproAM aa

Tyr-Gly-Gly attached at the N-terminus, P072 represents preproAM ac

116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
for the prevention and/or treatment of cancers, e.g. adrenal, nervous
system, lung, colon, ovarian and breast cancer by inhibiting cell
for the prevention and therefore for treating and/or preventing diabetes
system, lung, colon, ovarian and breast cancer by inhibiting cell
flowers metabolism and therefore for treating and/or preventing diabetes
type II. They may be used for the diagnosis or treatment of conditions
to predict the following: (i) regulating neurotransmission or neuron growth in
areas of the central nervous system; (ii) lessening or inhibiting mast
cell degranulation and hence reducing the effects of an allergic
response, (iii) inhibiting or preventing bacterial and fungal growth (to
creat and hence reducing the effects of an allergic
creat and hence and an enventing bacterial and fungal growth (to
creat and hence and and process the second or promoting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component; modification; succinimidyl, maleimido group; amino, hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         Human adrenomedullin peptide(s), P070, P071, P072 and PAMP-20 - used in the diagnosis and treatment of type II diabetes and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thibaudeau K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                        Martinez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 163; DB 18; Local Similarity 100.0%; Pred. No. 1.9e-18; nes 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmes DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TVQKLAHQIYQFTDKDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adrenomedullin peptide (AM) SEQ ID NO:938.
                                       Cuttitta F, Gray K, Hook W, Macri C,
Miller MJ, Unsworth EJ, Walsh T;
              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bridon DP, Ezrin AM, Milner PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB91762 standard; Peptide; 31 AA
                                                                                                                                                  Claim 1; Page 43; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0134406.
99US-0153406.
99US-0159783.
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                                                                                                                                                                                                                                                                                                                                                                                                                 organ and bone development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                               WPI; 1997-165298/15
                                                                                                                                                                                                                                                                                                                                                                                                                                            31 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200069900-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAY-1999;
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15-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB91762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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The present invention describes a modified therapeutic peptide (I) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinindly) and malelmido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide components to form a component of the amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treament of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the hody.

Wodifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life and specificity as bonding to large molecules decreases that intracellular uptake and interference with physiological processes.

AMB90829 to AAB92441 represent invention.
Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
CGRP-receptor identification; adrenomedullin.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 163; DB 22;
100.0%; Pred. No. 1.9e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                      Disclosure; Page 499-500; 733pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE09827 standard; peptide; 31 AA.
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Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCR-) UNIV CREIGHTON.
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Gaps

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Indels

Length 52;

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comprising a therapeutically active amino acid region [III] and a reactive group [II] (e.g. succinimidyl and maleimido groups) attached to a leactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region [IV], which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half infracellular uptake and interference with physiological processes. ARB908129 to AAB92441 represent peptides which can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protection, endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a modified therapeutic peptide (I)
     100.0%; Score 163; DB 22; 100.0%; Pred. No. 3.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holmes DL,
                                                                                                                                   22 TVQKLAHQIYQFIDKDKDNVAPRSKISPQGY 52
                                                                                                         1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31.
                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Adrenomedullin peptide (AM) SEQ ID NO:935.
                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 498; 733pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milner PG,
                                                                                                                                                                                                                                                                                 AAB91759 standard; Peptide; 52 AA.
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99US-0153406.
99US-0159783.
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                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ezrin AM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-112059/12.
                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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                                                         31;
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                                                                                                                                                                                                                                                                                                                                      AAB91759;
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       Query Match
Best Local
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                                                    Matches
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AAB91759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                    The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a member of the CGRP-receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intercells either in vitro or in vivo to inhibit the effect of CGRP adrenomedullin peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitsushima K;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 163; DB 22; 100.0%; Pred. No. 1.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 45; 75pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human adrenomedullin (AM) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB75110 standard; Protein; 52 AA
                       Column 6; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-0CT-2000; 2000WO-JP07023.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    31; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      31 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-0CT-1999;
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                                                                                                                                                                                                                                                                                                                                                      Sequence
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                     Claim 5;
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Thibaudeau K;

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                                     Gaps
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       Length 52;
                                 Indels
   100.0%; Score 163; DB 22;
100.0%; Pred. No. 3.6e-18;
ive 0; Mismatches 0;
                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Query Match
Best Local Similarity 100.
Matches 31; Conservative
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us-09-931-700-3.rag

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Homo sapiens
                                                                                                                                      Zurdo J,
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                                                                                                                                                                                                                                                                                                                              The invention relates to antagonists of the vasoactive peptide calcitonin gene related peptide (CGRP) and other members of the CGRP superfamily. The invention also relates to amino the terminal modifications of peptides to improve their ability to bind to a nember of the CGRP receptor super-family. CGRP antagonists are used for inhibiting CGRP activity which can be used in vitro e.g. in assays to identify and/or isolate CGRP receptors or with intact calls either in vitro or in vivo to inhibit the effect of CGRP binding to its receptor. The present sequence is human adrenomedullin peptide.
                                                                                                                     Human; vasoactive peptide; calcitonin gene related peptide; CGRP; CGRP-receptor identification; adrenomedullin.
                                                                                                                                                                                                                                                                                      Vascactive peptides useful for inhibiting calcitonin gene related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 163; DB 22;
Pred. No. 3.6e-18;
22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                               Claim 5; Column 25-26; 24pp; English.
                                               AAE09818 standard; peptide; 52 AA.
                                                                                                   Human adrenomedullin peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
100.0%;
                                                                                                                                                                                                    98US-0070504
                                                                                                                                                                                                                                                       Saha S, Abel PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP55104 standard; Peptide;
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                              peptide receptor activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Conservative
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Best Local Similarity
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                                                                                                                                                                US6268474-B1
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                                                                                                                                                                                                                                                     Smith DD,
                                                                  AAE09818;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                RESULT 6
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ABP55104
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The present sequence is that of human adrenomedullin, a potent hypotensive and vasodilator. The invention provides modified calcitonin and related peptides, such as adrenomedullin, that have at least 70% identify to the native form but are modified such that the tendency of the peptide to aggregate is reduced. Preferred regions for modification include those for which the peptide is polymorphic amongst different species, which increase the propensity of the peptide to form local interactions of the peptides or increase the net charge of the peptide. When aggregation is reduced to prevented, lower doses of the drug can aggregation is reduced to prevented, lower doses of the drug can be used. Side-effects and undesired responses are minimised by retaining high sequence identity to the human peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New modified human calcitonin peptide having reduced aggregation, useful for the treatment of Paget's disease, hypercalcemia and/or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 163; DB 24;
100.0%; Pred. No. 3.6e-18;
Five 0: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 52
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Location/Qualifiers 16..21
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                                                                                                                                                                                            17-APR-2002; 2002WO-GB01778.
                                                                                                                                                                                                                                                      17-APR-2001; 2001GB-0009438.
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                                                                                                                                                                                                                                                                                                                                                                               Dobson CM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 AA;
                  Disulfide-bond
                                                                             WO200283734-A2
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                                                                                                                                       24-OCT-2002
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(first entry)
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                                                                                                                    Local Similarity
Les 31; Conserv
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                                                                                     53 AA;
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                                                                                                                                                                                                                                                                                                                                                Unidentified.
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                                                                                       Seguence
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Matches
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                                                                                                                                  and advanced to the production describes a method (M1) for producing development of a direnomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications, AAN19806 to AAN19806 and AAN75110 to AAN75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused
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                                                                       Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a
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                      Mitsushima K;
                                                                                                                                                                                                                                                                  Score 163; DB 22;
Pred. No. 3.7e-18;
0; Mismatches 0;
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                      Nakayama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 47; 75pp; Japanese.
                                                                                                                 Example 1; Page 46; 75pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                       A.
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100.0%;
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                      Mitsuda Y,
(SHIO ) SHIONOGI & CO
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                                         WPI; 2001-282044/29.
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                               53 AA;
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                                                                                              recombinant host
                                                    N-PSDB; AAH19807
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Best Local Simil
Matches 31; C
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                     Takimoto A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 repersent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 3.7e-18;
Mismatches 0;
                                                                                                                                                                                                                                                                                              Score 163; DB 22;
Pred. No. 3.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52
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100.0%;
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AAB75113;

RESULT 11 AAB75113

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The present invention describes a method (M1) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAB15110 to AAB75110 to AAB775110 to AAAF775110 to AAA775110 to AAA775110 to AAA775110 to AAA775110 to A
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host.
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                                                                                                                                                                                                                                                                                                                       Nakayama T, Mitsushima K;
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100.0%; Pred. No. 9.9e-18;
iive 0; Mismatches 0;
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N-PSDB; AAH19864.
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es 31; Conserv
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                                                                                                      19-APR-2001
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  Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method (MI) for producing adrenomedullin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedullin precursor. The method can be used for the production of adrenomedullin precursor for pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                   Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly; adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
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                                                                                                                                                                                                                               Linker peptide-adrenomedullin (AM) precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitsushima K;
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Pred. No. 4.5e-18;
Mismatches 0;
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100.0%; Pred. No. 4...
0; Mismatches
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                                                                    AAB75113 standard; Protein; 62 AA.
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Best Local Similarity 100.0
Matches 31; Conservative
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Sequence

AAB75122;

RESULT 12 AAB75122

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Length 120;

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Query Match
Best Local Similarity
     120 AA;
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                                                                                                                                                                                                                                                                 Fusion peptide;
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                                                                                                                                                                                                                                                                                                   Unidentified.
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      Sequence
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                                                                                          The present invention describes a method (MI) for producing adrenomedulin precursor. The method comprises: (a) producing the fused protein using a recombinant host cell; (b) restricted digestion of the fused protein by a protease followed by collection of sediment; and (c) dissolving the sediment and extracting adrenomedulin precursor. The method can be used for the production of adrenomedulin precursor for pharmaceutical and diagnostic applications, AAH19806 to AAH19866 and AAB75110 to AAB75124 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
                     Producing adrenomedullin useful for pharmaceutical and diagnostic application comprises producing fused adrenomedullin precursor using a recombinant host \dot{\,}
                                                                                                                                                                                                                                                                           Gaps
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large scale peptide production.
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100.0%; Pred. No. 9.9e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                            1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                    Claim 17; Page 69-70; 75pp; Japanese.
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                                                                                                                                                                                                                                                          Best Local Similarity
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N-PSDB; AAH19865
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                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion polypeptide of Escherichia coli universal stress peptide with a target peptide, useful for efficient large scale production of the target peptide comprising expression of the fusion polypeptide followed
                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 universal stress peptide; UspA; linker peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 120;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                              Universal stress protein A (uspA)-related protein #5.
Score 163; DB 24;
Pred. No. 9.9e-18;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 163; DB 24; 100.0%; Pred. No. 9.9e-18;
                                                                                                                  1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            October 14, 2003, 08:38:47
                                                                                                                                                                                                                                                      ABJ18670 standard; Protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 5; Page 38; 49pp; Japanese.
  100.08; FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       large scale peptide production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-2002; 2002WO-JP03374,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001JP-0111088,
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SHIO ) SHIONOGI & CO LTD.
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-067581/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: Octobe
Job time : 53.1364 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 AA;
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
```

- protein search, using sw model OM protein October 14, 2003, 08:36:56; Search time 17.6136 Seconds (without alignments) 169.257 Million cell updates/sec Run on:

US-09-931-700-3 Title: Perfect score:

163 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries pirl:\* pir2:\* pir3:\* pir4:\* PIR\_76:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Description              | enomedullin p | adrenomedullin - p | in pr  | hypothetical prote | hypothetical prote | S-locus-specific g | S-locus-specific g | lipopolysaccharide | hypothetical prote | S-locus-specific g | S-locus-specific g | S-locus-specific g | S-locus-specific g | probable S-recepto | hypothetical prote | ific   | ific   | S-locus-specific g | -locus-specific | tor kinase | S-locus-specific g | -locus | -locus-spec |        | hypothetical prote |        | glycylpeptide N-te | บ      | histidine-tRNA lig |
|--------------------------|---------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|-----------------|------------|--------------------|--------|-------------|--------|--------------------|--------|--------------------|--------|--------------------|
| QI.                      | JN0684        | S41600             | JN0766 | A99638             | 48                 | 53                 | T14415             | 10                 | 10                 |                    | T07814             |                    | A27827             | T14471             | C86279             | T14424 | T14423 | T14416             | T14530          | T07809     | T14528             | T07812 | 7           | S04906 | T47067             | AG0363 | C134               | T07810 | 6913               |
| Length DB                | 185           |                    | 185 2  |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |                    |        |        |                    |                 |            |                    |        |             |        |                    |        |                    |        |                    |
| \$<br>Query<br>Match Len | 100.0         | ε.                 | 8.0    | 6.                 | 5.9                | 5.6                | 4                  | 3.1                | 5                  | 1.9                | 1.3                | ۳.                 | ۳.                 | ۳.                 | 7.1                | 7.0    | 7.0    | 30.1               | 0.1             | 0.1        | 1.0                | _      | 0.1         | 0.1    | 9.8                | 9.4    | 4.6                | 4.6    | 9.4                |
| Score                    | ~             | 157                | 148    | 58.5               | œ                  | 58                 | 99                 | 54                 | 53                 | 52                 | 51                 | 51                 | 51                 | 51                 | 50                 | 20     | 20     | 49                 | 49              | 49         | 49                 | 49     | 49          | 49     | 48.5               | 48     | 48                 | 48     | 48                 |
| Result<br>No.            | П             | 7                  | m      | 4                  | ស                  | 9                  | 7                  | 80                 | 6                  | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16     | 17     | 18                 | 19              | 20         | 21                 | 22     | 23          | 24     | 25                 | 26     | 27                 | 28     | 29                 |

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Gaps

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ch 100.0%; Score 163; DB 2; Length 185; 1 Similarity 100.0%; Pred. No. 2.3e-16; 31; Conservative 0; Mismatches 0; Indels (

Query Match Best Local Similarity Matches 31; Conserv

| excinuclease ABC c | S-receptor kinase | S-receptor kinase | hypothetical prote | DNA primase (EC 2. | S-locus-specific g | flagellar M-ring p | hypothetical prote | S-receptor kinase | S-receptor kinase | transposase In4652 | high density lipop | canalicular multid | UDP-3-0-[3-hydroxy | hypothetical prote | hypothetical prote |
|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S39531             | JC2482            | JC2481            | F71414             | A55070             | T14524             | A84938             | T33517             | T14472            | JQ1677            | S51133             | A44125             | S71839             | S41752             | H90448             | C97389             |
| ~                  | Н                 | H                 | 7                  | ď                  | 7                  | ď                  | N                  | 7                 | H                 | ď                  | ~                  | Н                  | ~                  | N                  | 77                 |
| 689                | 856               | 828               | 1705               | 438                | 429                | 545                | 549                | 850               | 828               | 1004               | 1268               | 1541               | 340                | 186                | 204                |
|                    |                   |                   |                    |                    |                    |                    |                    |                   |                   |                    |                    |                    |                    |                    |                    |
| 29.4               | 29.4              | 29.4              | 29.4               |                    |                    |                    |                    |                   |                   |                    | 28.8               | 28.8               | 28.5               | 28.2               | 28.2               |
| 48 29.4            | 48 29.4           | 48 29.4           | 48 29.4            |                    |                    |                    | 47 28.8            |                   |                   |                    | 47 28.8            | 47 28.8            | 46.5 28.5          |                    | 46 28.2            |

## ALIGNMENTS

```
A; Cross-references: GDB:217070; OMIM:103275
A; Map position: llpter-llqter
A; Intros: 33,2; 83,2
A; Map position: llpter-llqter
A; Intros: 33,2; 83,2
C; Keywords: amidated carboxyl end; blood pressure control; hormone
C; Keywords: amidated carboxyl end; blood pressure control; hormone
E; 1-21/Domain: signal sequence #status predicted <PGD>
E; 22-41/Domain: proadrenomedullin astatus predicted <PED>
E; 22-41/Domain: carboxyl-terminal 20 peptide #status predicted <PAP>
F; 147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 110-115/Disulfide bonds: #status experimental
F; 146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
F; 146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 22-41 <KIZ>
R; Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
R; Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
B; Cochem. Biophys. Res. Commun. 192, 553-560, 1993
A; Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A; Reference number: JN0476
A; Molecule type: protein
A; Residues: 95-146 <KIS>
A; Residues: 95-146 <KIS>
A; Residues: 95-146 <KIS>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-185 <1SH>
A; Residues: 1-185 <1SH>
A; Residues: 1-185 <1SH>
A; Residues: 1-185 <1SH>
A; Cross-references: GB:S73906; NID:9765329; PIDN:AAC60642.1; PID:9765330
A; Experimental source: phecchromocytoma
B; Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem: Biophys. Res. Commun. 134, 720-725, 1993
A; Fille: Cloning and characterization of EDNA encoding a precursor for human adrenome
A; Reference number: JN0684; MUID:93343928; PMID:7688224
                                            C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-7eb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Date: 03-7eb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C;Accession: JC2351; JN0664; PN0548; JN0476
R;Ishimitsu, T; Kojima, M.; Kangawa, K.; Hino, J.; Matsuoka, H.; Kitamura, K.; Eto, Biochem. Blochem. Res. Commun. 203, 631-639, 1994
Biochem. Blochys. Res. Commun. 203, 631-639, 1994
A;Itile: Genomic structure of human adrenomedullin gene.
A;Reference number: JC2351; MUID:94354869; PMID:8074714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
adrenomedullin precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-185 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: PN0548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: JN0684
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC2351
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b

and

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C; Species: Escherichia coll.
C; Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001
C; Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 14-Sep-2001
C; Date: 185489
C; Accession: AB5489
Nature 409, 529-533, 2001
A; Title Genome sequence of enterohemorrhagic Escherichia coll 0157:H7.
A; Reference number: AB5489; MUID: 21074935; PMID: 11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE005174; NID:g12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:D85212; NID:92351155; PIDN:BAA21946.1; PID:92351156
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Z0078 [imported] - Escherichia coli (strain 0157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                        A;Cross-references: GB:BA000007; PIDN:BAB33496.1; PID:913359529; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Decies: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A; Accession: 114536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.9%; Scur.
34.4%; Pred. No. v...
... 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KLAHQIYQFTD-----KDKDNVAPRSKISPQG 30
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                                                                                                                                                                                                                                                                                                                                                                                       Score 58.5; D
Pred. No. 0.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                     A,Gene: ECs0073
C,Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: Escherichia coli yabP protein
                                                                                                                                                                                                                                                                                                                                                                                     35.9%;
ilarity 34.4%;
Conservative
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A;Molecule type: DNA
A;Residues: 1-189 <STO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                              A; Status: preliminary
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C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Dates 30-59-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C; Accession: JN0766; PN0610
R; Sakata, J; Shimokubo, T; Kitamura, K; Nakamura, S; Kangawa, K; Matsuo, H; Eto, T
Biochem: Biophys: Res Commun. 195, 921-927, 1993
A; Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensiv
A; Reference number: JN0766; MUID:93384621; PMID:7690563
A; Molecule type: mRNA
A; Residues: 1-186 SAK>
A; Accession: PN0610
A; Molecule type: protein
A; Residues: 22-41
C; Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin A; Residues: 22-41
C; Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin A; Residues: 22-41
C; Comment: Signal sequence #status predicted <PEU>F; 22-41/Product: proadrenomedullin maino-terminal 20 peptide #status predicted <PEU>F; 22-41/Product: proadrenomedullin #status predicted <AMAT>F; 24-1/Product: adrenomedullin #status predicted <AMAT>F; 24-1/Product: adrenomedullin #status predicted <AMAT>F; 24-1/Product: amidated carboxyl end (Tyr) (amide in mature form from following gly F; 143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly F; 143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                          hypothetical protein ECs0073 [imported] - Escherichia coli (strain 0157:H7, substrain RI C;Species: Escherichia coli ("Species: Escherichia coli ("Species: B-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 ("Accession: A99638 "R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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A;Molecule type: mRNA
A;Residues: 1-188 <KII>>
A;Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 157; DB 2; Le
Pred. No. 1.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 148; DB 2; Li
Pred. No. 3.7e-14;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 TVQKLAHQIYQFTDKDKDNYAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                               TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%;
96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 90.8%; ll Similarity 87.1%; 27; Conservative :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 96.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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us-09-931-700-3.rpr

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714529
714529
714529
S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (*11d cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14529
R;Kusaba, M; Nishio, T; Satta, X; Hinata, K; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A;Title: Striking sequence similarity in inter- and intra-specific comparisons of cl
                                                                                                                                A,Molecule,type: DNA
A,Residues: 1-465 <DUZ>
A,Cross-references: EMBL:U41279; NID:g1086905; PID:g1086919; PIDN:AAB52685.1; GSPDB:G
A,Experimental source: strain Bristol N2; clone C17C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;cross-references: EMBL:D85205; NID:92351141; PIDN:BAA21939.1; PID:92351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: SIG(S6)
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;32-426/Domain: S-locus-specific glycoprotein homology <SSG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SLG) and the S-locus related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Raphanus sativus (radish)
C.Species: Raphanus sativus (radish)
C.Species: Raphanus sativus (radish)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C.Accession: TOR14
R.Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998
A.Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus re A.Reference number: Z16146; MUID:98311079; PMID:9648745
A.Accession: T07814
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-428 <SAK>
A.Residues: 1-428 <SAK>
A.Conetics: EMBL:AB009682; NID:93327849; FIDN:BAA31729.1; FID:93327850
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                                                                                                                                                                                                                                                                                                                                                                            Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 52; DB 2; Length 428
Pred. No. 11;
8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 OKLSYMVYNETENSEEVAYTFRMTNNSFYSRLKVSSDGY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           echanism.
A;Reference number: 218078; MUID:97352858; PMID:9207151
A;Accession: T14529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-428 <KUS>
submitted to the EMBL Data Library, November 1995
A; Description: The sequence of C. elegans cosmid C17C3.
A; Reference number: Z18366
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                                                                               A; Accession: T15540
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                         Score 53; DB;
Pred. No. 8.7;
7; Mismatches
                                                                                                                                                                                                                                                                                            A; Map position: 2
A; Introns: 124/2; 138/2; 174/2; 223/1; 369/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 QEIAHKFEDFTELKKDSFSP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 OKLAHQIYQFTDKDKDNVAP 22
                                                                                                                                                                                                                                                                                                                                                                         32.5%;
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28.2%;
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8; Conserva
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nes 11; Conserv
                                                                                                                                                                                                                                                                    A; Gene: CESP:C17C3.1
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Best Local S
Matches 11
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Best Local S
Matches 8
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K; Wusaba, M; Nishlo, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S. A. 94, 7673-7678, 1997
A; Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07382.1; GSPDB:GN00
A,Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Uppoolysaccharide blosynthesis BH3663 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Date: 01-bec-2000 #sequence_revision 01-bec-2000 #text_change 15-Jun-2001 C; Accession: G84107 R; Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Reference number: A83650; MUID:20512582; PMID:11058132 A; Accession: G84107 A; Status; preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: 218078; MUID:97352858; PMID:9207151
A; Accession: T14415
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-431 <KUGS>
A; CLOUSS references: EmBL:D85215; NID:92351161; PIDN:BAA21949:1; PID:92351162
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
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C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 *sequence_revision 20-Sep-1999 *text_change 20-Sep-1999
C;Accession: T15540
R;Du, 2.
                                                                                                                                                                                                                                                                                                                     N;Alternate names: S glycoprotein
C;Species: Brassica rapa (turnip)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                         10;
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Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 QKLNYMVYNFTENSEDVAYTFRWTNKSIYSRLKISSEGF 270
                                                                                                                                                            230 EKLSYMVYNFTENNEEVAYTFRMTNNSIYSRLTVSPEGY 268
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                                                                                                          3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                         7;
        2;
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4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 2;
Pred. No. 2.9;
8; Mismatches
                                                                                                                                                                                                                                                                                            S-locus-specific glycoprotein - turnip (fragment)
                                                    12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
     Score 58;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 54;
Pred. No.
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     35.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.4%;
30.8%;
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48.08;
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Best Local Similarity 30.8 Matches 12; Conservative
                                                      10; Conservative
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Best Local Similarity
Matches 12; Conserv
     Query Match
Best Local Similarity
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A; Residues: 1-373 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: BH3663
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                                                         Matches
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hypothetical protein F14L17.23 [imported] - Arabidopsis thaliana C. Species: Arabidopsis thaliana (mouse-ear cress) C. Species: Arabidopsis thaliana (mouse-ear cress) C. Species: Arabidopsis thaliana (mouse-ear cress) C. Sates: Ochwar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C. Accession: C86Z79 C. M. Chung, M.R.; Conn, C. Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.E.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia A; Authors: Salzaberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Accession: C86Z79 A; Eatus: Preliminary A; Carls Davis, Preliminary A; Carls Davis, Davis
    Plant J. 6, 807-813, 1994
A;Title: Expression of the S-locus receptor kinase multigene family in Brassica olera A;Reference number: 218108; MUID:95152555; PMID:7849754
A;Accession: T14471
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: implicated in the self-incompatibility system of Brassica oleracea C; Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase; signal F; 41-436/Domain: S-locus-specific glycoprotein homology <SSG>
F; 526-813/Domain: protein kinase homology <KIN>
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A; Residues: 1-90 <STO>
A; Cross-references: GB:AE005172; NID:g7262688; PIDN:AAF43946.1; GSPDB:GN00141
C; Genetics:
                                                                                                                                                                                                                                                         A; Residues: 1-657 < KUM>
A;Cross-references: EMBL:230211; NID:9459244; PIDN:CAA82930.1; PID:9459245
A; Experimental source: strain alboglabra; stigma
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 2; Length 857
Pred. No. 34;
8; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 QKLSYMVYNFTQNSEEVVYTFRMTNNSIYSRLIISSEGY 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 QKLAHQIYQFTDKDKD-----NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 438/1; 481/1; 544/3; 615/1; 694/2; 744/3 C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IVQTIARPFIDETDKIQIVPYPPSKHTPPGY 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: October 14, 2003, 08:40:50 Job time : 19.6136 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.38;
28.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 28.2 tes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
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                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: srk29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: T14533
R; Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A; Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
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A.70st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: 218078; MUID:97352858; PMID:9207151
A;Accession: T14533
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-429 <KUS>
A;Cross-references: EMBL:D85209; NID:92351149; PIDN:BAA21943.1; PID:92351150
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C;Keywords: glycoprotein
                                                                                           ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                            S-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable S-receptor kinase (EC 2.7.1.-) srk29 - wild cabbage C;Species: Brassica oleracea (wild cabbage) C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                       10;
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        Length 428;
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16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 436;
16;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 QKLSYMVINFTENSEEVAYTFLMTNNSIYSRLTISSSGY 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QKLAHQIYQFTDKDKDNVA------PRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QKLAHQIYQFTDKDKD-----NVAPRSKISPQGY 31
                                                                                       10;
        DB 2;
    Score 51; DB 2
Pred. No. 16;
8; Mismatches
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31.3%; Score 51; DB:
Best Local Similarity' 25.6%; Pred. No. 16;
Matches 10; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.3%; Score 51; 32.5%; Pred. No. 3
                                                                                   .
8
    31.3%;
28.2%;
                                                                                                                                                             3 OKLAHQIYQFTDKDKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.5%
Matches 13; Conservative
                                                                                   Conservative
                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T14471
R; Kumar, V.; Trick,
Query Match
Best Local Simi
Matches 11;
                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 14, 2003, 08:35:36; Search time 9.86364 Seconds (without alignments) 147.798 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-931-700-3 163 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SwissProt\_41:\* Database :

# SUMMARIES

|           |        | Description | P35318 homo sapien | sas      | 7559 cani  |          |            |            | Q8g3h2 bifidobacte |              |           |            | P55521 rhizobium s | P58492 yersinia pe |           | P30419 homo sapien | O70310 mus musculu | P31717 bos taurus |            |            |            | homo sap   |          |            |            |            |            | Q9pnn2 campylobact |            | P35736 saccharomyc |            |            | Q09390 caenorhabdi | ~    | P39965 saccharomyc |
|-----------|--------|-------------|--------------------|----------|------------|----------|------------|------------|--------------------|--------------|-----------|------------|--------------------|--------------------|-----------|--------------------|--------------------|-------------------|------------|------------|------------|------------|----------|------------|------------|------------|------------|--------------------|------------|--------------------|------------|------------|--------------------|------|--------------------|
| SUMMARTES | ;      | ID          | ADML_HUMAN         | ADML_PIG | ADML_CANFA | ADML_RAT | ADML_BOVIN | ADML_MOUSE | ILVD_BIFLO         | SLS6_BRAOL   | VG48_BPMU | SLS2_BRAOA | Y4KA_RHISN         | ZIPA_YERPE         | SYH_METTH | NMT1_HUMAN         | NMT1_MOUSE         | NMT1_BOVIN        | UVRA_PSELE | PRI1_DROME | FLIF_BUCAI | VGLN_HUMAN | MRP2_RAT | LPXD_YEREN | DNAB_RHOMR | SLS3_BRAOL | SPAC_BACSU | GATA_CAMJE         | MIG6_MOUSE | YKFO_YEAST         | MRP2_HUMAN | PKSK_BACSU | HG12_CAEEL         | - 1  | SYPC_YEAST         |
|           | ,      | 80 ;        | 7                  | М        | Н          | П        | Н          | Н          | r-1                | ч            | Н         | H          | rH                 | Н                  | Н         | П                  |                    | 7                 | _          | -          | <b>—</b>   | Н          | -        | Н          | -          | -          | Н          |                    | Н          | Н                  | -          | H          | Н                  | Н    | П                  |
|           | 1      | Length      | 185                | 188      | 188        | 185      | 188        | 184        | 620                | 436          | 180       | 435        | 322                | 328                | 425       | 496                | 496                | 497               | 689        | 438        | 545        | 1268       | 1541     | 338        | 941        | 434        | 441        | 453                | 461        | 922                | 1545       | 4447       | 235                | 459  | 576                |
| dР        |        | Match       | 100.0              | 96.3     | 93.3       | 8.06     | 89.6       | 85.9       | 31.6               | 31.3         | 30.1      | 30.1       | 29.8               | 29.4               | 29.4      | 29.4               | 29.4               | 29.4              | 29.4       | 29.1       | 28.8       | 28.8       | 28.8     | 28.5       | 28.5       | 28.2       | 28.3       | 28.2               | 28.2       | 28.2               | 28.2       | 28.2       | 27.6               | 27.6 | 27.6               |
|           | 1      | Score       | 163                | 157      | 152        | 148      | 146        | 140        | 51.5               | 51           | 49        | 49         | 48.5               | 4 8                | 48        | 48                 | 48                 | 48                |            | 47.5       | 47         | 47         |          | 46.5       | 46.5       | 46         | 46         | 46                 | 46         | 46                 | 46         | 46         | 45                 | 45   | <b>₹</b>           |
|           | Result | NO.         | 7                  | 7        | ĸ          | 4        | ហ          | 9          | 7                  | <b>3</b> 0 · | o,        | 10         | 11                 | 12                 | 13        | 14                 | 15                 | 16                | 17         | 18         | 91.        | 20         | 21       | 22         | 23         | 7.7        | 25         | 26                 | 27         | 28                 | 29         | 30         | 31                 | 32   | 33                 |

| P44894 haemophilus<br>P38132 saccharomyc | P54697 dictyostell P35194 saccharomyc | P55824 drosophila | Q9qzz4 mus musculu | Q9ukn7 homo sapien | Q96zd7 sulfolobus | 09ya42 aeropyrum p | Q12541 agaricus bi | Q12542 agaricus bi | P36285 san miguel |
|--|---------------------------------------|-------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|
| FRDA_HAEIN<br>CC47_YEAST                 | MYSJ_DICDI<br>YBA4 YEAST              | FAF_DROME         | MY15_MOUSE         | MY15_HUMAN         | GCS3_SULTO        | YK96_AERPE         | LAC1_AGABI         | LAC2_AGABI         | COAT_SMSV4        |
| 599 1<br>845 1                           | 2245 1<br>2493 1                      | 2778 1            | 3511 1             | 3530 1             | 136 1             | 426 1              | 520 1              | 520 1              | 703 1             |
| 27.6                                     | 27.6                                  | 27.6              | 27.6               | 27.6               | 27.3              | 27.3               | 27.3               | 27.3               | 27.3              |
| 45<br>45                                 | 4 4<br>7 1                            | 45                | 45                 | 45                 | 44.5              | 44.5               | 44.5               | 44.5               | 44.5              |
| 34<br>35                                 | 36<br>37                              | 38                | 39                 | 40                 | 41                | 42                 | 43                 | 44                 | 45                |

# ALIGNMENTS

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VARIANT
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                                                                               Matches
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                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                         -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR AGENTS. NUMBEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE PHYSIOLOGIC CONTROL OF FULID AND ELECTROLYTE HOMOSTASIS. IN THE KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN PITILITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME, ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
                                                                                                                                                                                        MEDITINE=20053666, PubMed-10588445;
Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
"Structure-activity relationships of adrenomedullin in the circulation
                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION (G-42 PROVIDE AMIDE GROUP).

AMIDATION (G-147 PROVIDE AMIDE GROUP).
                                    Matsuo H., Eto T.; "Adrenomedullin: a novel hypotensive peptide isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hormone; Amidation; Cleavage on pair of basic residues; Signal;
            MEDLINE-93249425; PubMed-8387282;
Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREPROAM C-TERMINAL FRAGMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005625; C:soluble fraction; TAS.
GO; GO:000611; P:caMP biosytthesis; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007565; P:pregnancy; TAS.
GO; GO:000765; P:pregnancy; TAS.
GO; GO:000611; P:response to wounding; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPRO01710; Adrenomedullin.
                                                               pheochromocytoma.";
Biochem. Biophys. Res. Commun. 192:553-560(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADRENOMEDULLIN.
                                                                                                                                      "Proadrenomedullin-derived peptides.";
Front. Neuroendocrinol. 19:100-127(1998).
                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; BC015961; AAH15961.1; -.
EMBL; D43639; BAA07756.1; ALT_SEQ.
PIR; JC2351; JN0684.
                                                                                                              MEDLINE=98240137; PubMed=9578982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D14874; BAA03589.1; -. EMBL; S73906; AAC60642.1; -.
                                                                                                                                                                                                                                and adrenal gland.";
Regul. Pept. 85:1-8(1999).
TISSUE=Pheochromocytoma;
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125
125
146
146
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                                   Eto T.;
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                                                                                                                              Samson W.K.;
                                                                                                                                                                                                                                                                                                                                                                             VESSELS
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Adrenal medulla;
MEDLINE-94139945; PubMed-8043068;
Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
"Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding its precursor.";
FEBS Lett, 338:306-310(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 22-41.

TISSOE-Adrenal medulla;

MEDLINE-9437274; PubMed-8076689;

Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,

Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,

Kawamoto M., Minamino N., Matsuo H., Eto T.;

Iidentification and hypotensive activity of proadrenomedullin

N'-terminal 20 peptide (PAMP).";

FEBS Lett. 351:35-37(1994).

-: FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP).
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                         Length 185;
                                                                                                                                                              Indels
S -> R (in dbSNP:5005).
/FTId=VAR_014861.
64C7D2A0B4654DFE CRC64;
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                                                                                                 100.0%; Score 163; DB 1; 100.0%; Pred. No. 4.2e-16;
                                                                                                                                                                                                                                      188 AA
                                                                                                                                                                                                             1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                        0; Mismatches
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PIR; S41600; S41600.
InterPro; IPR001710; Adrenomedullin.
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                                                  185 AA; 20420 MW;
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
  20
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188
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                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
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                                                                                                      Query Match
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PIR; JN0766;
InterPro; IP
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Ono Y., Kojima M., Okada K., Kangawa K.;
"cDNa Cloning of canine adrenomedullin and its gene expression in the
mart and blood vessels in endotoxin shock.";
Shock 10:243-247(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HORMONE; Amidation; Cleavage on pair of basic residues; Signal.
SIGNAL 1 21 BY SIMILARITY.
PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                          Gaps
                                                                                                                                                                                                                077559; 09TVC9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
AMIDATION (G-147 PROVIDE AMIDE GROUP). 71749460F5660A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1 - FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
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AMIDATION (G-42 PROVIDE AMIDE GROUP)
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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                                            Length 188;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Imoto I., Jougasaki M.;
"Cloning of cDNA encoding canine adrenomedullin.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> K (IN REF. 2).
809D6A64F98F5578 CRC64;
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                                            DB 1;
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                                            Score 157; DB 1
Pred. No. 3e-15;
                                                                                                                    (BY SIMILARITY)
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                                                                                                                                                                                                       188 AA.
                                                                                                    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                        0; Mismatches
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BY SIMILARIT
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InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
                                                                                                                                                                                                       PRI;
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             20893 MW;
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                                            96.3%;
96.8%;
                                                                        30; Conservative
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                       Canis familiaris (Dog).
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146
188
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188 AA;
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Best Local Similarity
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                                                         Local Similarity
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SEQUENCE FROM N.A.
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MEDLINE-96102137; PubMed-8524787;
MEDLINE-96102137; PubMed-8524787;
MEDLINE-96102137; PubMed-8524787;
Mang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N., Sulpizio A.C., Aiyar N.V., Euffolo R.R. Jr., Feuerstein G.Z.;
Discovery of adrenomedullin in rat ischemic cortex and evidence for "Discovery of adrenomedullin in rat ischemic damage.";
Its role in exacerbating focal brain ischemic damage.";
Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
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                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM): Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Molecular cloning and biological activities of rat adrenomedullin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY, HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION (G-144 PROVIDE AMIDE GROUP)
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SIGNAL 1 21 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
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Indels
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35CAD9A9DD19AE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. Biophys. Res. Commun. 195:921-927(1993).
5
                                                   116 TVQKLAHQIYQFTDNDKDGVAPRSKISPQGY 146
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley, TISSUE-Adrenal gland; MEDLINE-93384621; PubMed-7690563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADRENOMEDULLIN
                                                                                                                                                         185 AA.
                                1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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Mismatches
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                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02039; Adrenomedullin; 1. PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
;
                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D15069; BAA03665.1; -. EMBL; U15419; AAB60519.1; -.
29; Conservative
                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypotensive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JN0766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matsuo H., Eto T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
45
94
149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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RESULT 6
ADML_MOUSE
                                                      SS THE THE THE THE THE TRANSPORT OF THE 
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                                                  Gaps
                                                                                                                                                                                                                                                       16-00T-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOTMONE; Amidation; Cleavage on pair of basic residues; Signal.

SIGNAL
1 21 BY SIMILARITY
PREPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
PROPEP 45 92 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barker S., Wood E., Clark A.T.L., Corder R.;
"Cloning of bovine preproadrenomedullin and inhibition of its basal
Life Sci. 62:1407-1415(1988).
-!-PUNCTION HYPOTENSTYE PEPTIDE. MAY FUNCTION AS A HORMONE IN
CIRCULATION CONTROL (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
AMIDATION (G-147 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARÍTY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
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            Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 188;
                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3002E79AB3B6612C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
      Score 148; DB 1;
Pred. No. 5.7e-14;
; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1e-13;
                                                                                                           188 AA.
                                                                               1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.6%; Score 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDULN.
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98244567; PubMed=9585168;
                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 AA; 20981 MW;
    90.8%;
87.1%;
                                            27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae; Bos.
NCBL_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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                                                                                                                                                                                                                                                                                                                                                                                 taurus (Bovine)
                           Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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les 28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IISSUE-Aorta;
                                                                                                                                                                                                                    ADML_BOVIN
062827;
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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PEPTIDE
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Matches
                                            Matches
                                                                                                                                                                                RESULT 5
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PRT; 184 AA.
P97297; P97453;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Expression of adrenomedullin, a hypotensive peptide, in the trophoblast giant cells at the embryo implantation site in mouse."; Dev. Biol. 203:264-275(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATATOR
                                                                                                                                                                                                               Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                    Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T., Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.; "Genomic organization, expression, and chromosomal mapping of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMIDATION (G-145 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
AMIDATION (G-42 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hormone; Amidation; Cleavage on pair of basic residues; Signal. SIGNAL 1 21 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREPROAM C-TERMINAL FRAGMENT (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 140; DB 1; Lengta -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> G (IN REF. 2),
C88C99045A79C898 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SÜBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADRENOMEDULLIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001710; Adrenomedullin.
Pfam; PF02039; Adrenomedullin; 1.
PRINTS; PR00801; ADRENOMEDUIN.
                                                                                                                                                                                                                                                                                                                         STRAIN-129/Sv;
MEDLINE-97092892; PubMed-8938454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE~99046755; PubMed=9808778;
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse adrenomedullin gene.";
Genomics 37:395-399(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D78349; BAA11367.1; -. EMBL; U77630; AAB36535.1; -.
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83.9%;
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nes 26; Conservative
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184
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InterPro; IPR001710;
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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45
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151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KO M.S.H.;
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eurosids II; Brassicales; Brassicaceae; Brassica.
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VG48_BPMU
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E E E E E E E
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                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                             MEDLINE-2294977; PubMed-12381787; Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni F.; "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal ract." Tact."

Proc. Natl. Acad. Sci. USA. 99:14422-14427(2002).

-I. CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica oleracea (Cauliflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00886; ILVD_EDD_1; 1.
PROSITE; PS00887; ILVD_EDD_2; FALSE_NEG.
Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ښ</u>
                                                                                                                                                    Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
; 463F654306027ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                   -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
-1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
-1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
S-locus-specific glycoprotein S6 precursor (SLSG-6).
                                                                      15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
10-ylydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
ILVD OR BL1788.
                                               620 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 12;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VVKIAHOYY---DDSDDSVLPRSIATKEAF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.6%; Score 51.5; 40.0%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAWAP; MF_00012; -; 1.
Pfam; PF00320; IIVVD=EDD; 1.
ProDom: P0002691; IIVVD EDD_family; 1.
TIGREAMS; TIGR00110; 11VD; 1.
                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE014813; AAN25571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620 AA; 66557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4Fe-4S; Complete proteome.
                                                                                                                                                                                                                                                                                                                                         oxobutanoate + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 40.09
Matches 12; Conservative
                                               STANDARD;
                                                                                                                                           Bifidobacterium longum.
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=216816;
                                              LIVE BIFLO
                                                                                                                                                                                                                        STRAIN-NCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLS6_BRAOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                              Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
Nature 326:523-523(1987).
-:- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
(THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
                                                 SEQUENCE FROM N.A.
Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
"Amino-acid sequence of glycoproteins encoded by three alleles of the
S locus of Brassica oleracea.";
                                                                                                                                                                                                                                           Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN B.OLERACEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.3%; Score 51; DB 1; Length 436; 25.6%; Pred. No. 9.5; ive 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Polymorphism; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2332635B885A515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 OKLSYMVYNFTENSEEVAYTFRMTNNSIYSRLTLSSEGY 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 OKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
16-CCr-2001 (Rel. 40, Last annotation update)
Protein gp48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A2782; A27827.
InterPro; IPR001480; B lectin.
InterPro; IPR001480; Bna_app.
InterPro; IPR001689; Slocus_glycop.
Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S_locus_glycop.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X03170; CAA68375.1; -. EMBL; X03170; CAA26934.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- TISSUE SPECIFICITY: STIGMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49779 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KINASE RECEPTOR (ZMPKI).
                                                                                                                                                                                                                    SEQUENCE OF 22-435 FROM N.A.
                                                                                                                                                               Nature 326:617-619(1987).
                                                                                                                                                                                                                                                                                                                                  Nature 318:263-267(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Self-incompatibility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 AA;
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NCBI_TaxID-3712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VG48_BPMU
Q9T1V1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                           oleracea
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Y4KA_RHISN
P55521;
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                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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            DOR KODOR KO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
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                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                      Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: INVOLVED IN SPOROPHÝTIC SELF-INCOMPATIBILITY SYSTEM (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea var. alboglabra (Chinese kale).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A homozygous S genotype of Brassica oleracea expresses two S-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -I- TISSUE SPECIFICITY: STIGMA.
-I- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN B.OLERACEA.
                      Bacteriophage Mu.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
Mu-like viruses.
                                                                                                                                                                 Morgan G., Hatfull G., Hendrix R.; "Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage FluMu.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.1%; Score 49; DB 1; Length 180; 62.5%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF083977; AAF01126.1; -.
SEQUENCE 180 AA; 20468 MW; 3045A6C185B48BF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
5-locus-specific glycoprotein BS29-2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      435 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gen. Genet. 218:112-117(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=89384424; PubMed=2550759;
Trick M., Flavell R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S04906; S04906.
InterPro; IPR001480; B_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 KPAHQIYKEVYHDGDN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 62.58
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=10677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3714;
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SLS2_BRAOA
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MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                           S-LOCUS-SPECIFIC GLYCOPROTEIN BS29-2.
N-LINKED (GLONAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizoblum and legumes."; Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid sym pNGR234a.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                Interior, introvers, sector processing the profile of the profile 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.1%; Score 49; DB 1; Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Plasmid.
SEQUENCE 322 AA; 36690 MW; 177B0AF61FA0C74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 OKLSYMVYNFIQNSEEVAYTFIMTNNSIYSRLTISSSGY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 18;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 VNKLADEI-QFTTKNSFSATPSAELDPANH 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence
01-NOV-1997 (Rel. 35, Last annotation
Hypothetical 36.7 kDa protein Y4KA.
InterPro; IPR003609; Pan_app.
InterPro; IPR000858; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49543 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium sp. (strain NGR234).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000081; AAB91733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                     30
                                                                                                                                                                                                                                                                                                                                                                                                                          113
120
244
260
389
435 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIPA_YERPE
P58492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIPA_XERPE
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NMT1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-Z2137865; PubMed=12142437.
MEDLINE-Z2137865; PubMed=1214243.
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Petherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 184:4601-4611(2002).

-1- FUNCTION: Interacts directly with the cell division protein ftsz.
Probable receptor for the septal ring structure, may anchor it to the inner-membrane (By slimilarity).

-1- SUBCELLULAR LOCATION: Type ID membrane protein. Inner membrane (By
                                                                                                                                                                                                                                                                                                 MEDLINE-21470413; PubMed-11586350;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Leatherl T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stewens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMÁR), MF 00509; -; 1.
Pfam; PF04354; ZipA_C; 1.
Cell division; Septation; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC (POTENTIAL).
EA04B89084649044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERIPLASMIC (POTENTIAL).
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
c28-FEB-2003 (Rel. 41, Last annotation update)
ZIPA OR YPO2990 OR Y1491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
-!- SiMiLARITY: Belongs to the zipA family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 VEKPAHOVAPQOHVESQOEPVAPAPEAKPQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of Yersinia pestis KIM.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VQKLAHQI--YQFTDKDKDNVAPRSKISPQ 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.4%; Score 48; 36.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AJ414154; CAC92234.1; -.
EMBL; AE013752; AAM85062.1; ALT_INIT.
                                                                                                                                                                                                                                                                                  / Biovar Orientalis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328 C
36098 MW;
                                                                                                                                                                              Enterobacteriaceae; Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 3
328 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; AG0363; AG0363
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                  Yersinia pestis
                                                                                                                                                                                                           NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Piterrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Juleario, Annocazo,
Pfam; PF03129; HGTP
Pfam; PF03129; HGTP
Pfam; PF03129; HGTP
Pfam; PF03129; HGTP
TIGRPAMs; TIGR00442; hiss; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; AIP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APT.1993 (Rel. 25, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase)
1) (NMT 1) (Type I N-myristoyltransferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                            30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                           Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 425; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425 AA; 48019 MW; 8388A5975A017535 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 EEVVNQIYHFTDKGGRELALRPELT 80
                                                                                                                                                              Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QKLAHQIYQFTDKDKDNVAPRSKIS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000811; AAB84750.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004154; HGTP_anticodon.
InterPro; IPR004516; Hiss.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR006195; tRNA_ligase_II.
                                                                                                                                                                                                                                                                                                                               STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.0%;
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15-JUL-1998 (Rel. 36, 30-MAY-2000 (Rel. 39, 28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; 032422; 1QE0.
HAMAP; MF_00127; -;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome
SEQUENCE 425 AA.
                                                                                                                                       HISS OR MTH244.
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425 AA.

PRT;

STANDARD;

SYH\_METTH 026346;

RESULT 13 SYH\_METTH

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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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            SO PRESENTANTA PROPERTY AND DESCRIPTION OF THE PROPERTY AND DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RACTURE AND Skin;

RACTURE STATES AND SHORT STATES AND SHORT).

REDINE-238825; PubMed-12477932;

REDINE-238825; PubMed-12477932;

REDINE-238825; PubMed-12477932;

RACTURE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RACTURE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RACTURE R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RACTURE R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RACTURE R. S., Loquellan R., Farmer A.A., Rubin G.M., Hong L.,

RACTURE R. S., Vorlan T.B., Toshiyut S., Carnincl P., Scheetz T.E.,

RACTURE R. S., Worley R.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RACTURE S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RICHARDS S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RALIAION D.K., Muray D.M., Schergren E.J., Lu X., Gibbs R.A.,

RALIAIN A., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RACTURE R. R., Touchman J.W., Scheurt J., Myers R.M.,

RACTIGUEZ A.C., Grimwood J., Schmutz J., Myers R.M.,

RACTIGUEZ A.C., Grimwood J., Schmutz J., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Shevchence S.T., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Shevchence S.T., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., A., Schein J.E., Shevchence S.T., Shevchence S.T., Shevchence S.T., Maria M.A.;

RACTURE A., Schein J.E., Jones S.J.M., Maria M.A.;

RACTURE A., Schein J.E., Shevchence S.T., Shevcher S.D., Shevcher S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blockem, J. 333:491-495(1998).
-!- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue of certain cellular and viral proteins.
-!- CATALITIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
                                                                                                                                            SECUENCE OF 58-496 FROM N.A., AND MUTAGENESIS OF GLY-492.
MEDIINE-92237320; PubMed=1570339;
Duronio R.J., Reed S.I., Gordon J.I., Gordon J.I., "Mutations of human myristoyl-Coahsrotenter furnansferase cause temperature-sensitive myristic acid auxotrophy in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-myristoyltransferase: evidence for an alternative splice variant of the enzyme.";
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glover C.J., Hartman K.D., Felsted R.L.; Human N.myristcoyltransferase amino-terminal domain involved in targeting the enzyme to the ribosomal subcellular fraction."; J. Biol. Chem. 272:28680-28689(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.-!- SIMILARITY: BELONGS TO THE NAT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Characterization of human and rat brain myristoyl-CoA:protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 81-89 FROM N.A.
MEDLINE-98343933; PubMed-9677304;
Mcilhinney R.A.J., Young K., Egerton M., Camble R., White A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                          cerevisiae.";
Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A second mammalian N-myristoyltransferase.";
J. Biol. Chem. 273:6595-6598(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId-P30419-2; Sequence-VSP_003570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P30419-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: CYTOPIASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-98019247; PubMed-9353336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98175914; PubMed=9506952; Giang D.K., Cravatt B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tetradecanoylglycyl-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-Short;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soloviev M.;
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Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
61yCylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Peptide N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase)
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MEDLINE-22388257; PubMed-12477932;

Strausberg R.L., Feingrold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

HOPKins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TVQKLAHQIYQFTD-------KDKDNVAPRSKISPQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform Short).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId-YSP_003570.
G->D,K: REDUCED ACTIVITY.
7661140D3837BE7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE: PS00975; NWT 1: 1.
PROSITE; PS00976; NWT 2: 1.
Transferase; Acyltransferase; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A second mammalian N-myristoyltransferase.";
J. Biol. Chem. 273:6595-6598(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB
Pred. No. 29;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 160993; -.
GO; GO:0009249; P:protein-lipoylation; TAS.
                                                                                                                                                                                                        EMBL; M86707; -; NOT_ANNOTATED_CDS.
EMBL; AF04334; AAC09294 1; ALT_INIT.
EMBL; AF020500; AAB95316.1; -.
EMBL; BC00658; AAB06538.1; -.
EMBL; BC00558; AAB06569.1; -.
EMBL; BC007288, AAB0558.1; -.
EMBL; BC007281; -.
EMBL; CO08312; AAB08312.1; -.
EMBL; CO08312; AAB08312.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Y17209; CAA76686.1; -. JC1343; JC1343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000903; Nmt. Pfam; PF01233; NMT; 1. Pfam; PF02799; NMT_C; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:7857; NMT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; JC1343; JC134;
HSSP; P30418; 1NMT
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070310;
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
R. Bosak S.A., McDean P.J., Wokeran K.J., Ablak J.A., Candrada S., Worlandon N.A., Macha M.A., Cay L.J., Hullyk S.W.,
R. Richards S., Worlandon D.K., Modergren B.J., Lu X., Gabs R.M.,
R. Richards S., Worlandon D.K., Mullandon M., Gay L.J., Hullyk S.W.,
R. Rahdy J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
R. Butterfield V.S. M., Krzywinski M.I., Skalsku U., Smallus D.E.,
R. Rochmeroh A. Scheint J.E., Jones S.J.M., Marra M.A. Smallus D.E.,
R. Pocon Matl. Acad Sci. U.S.A. 9916899-16903(2002);
R. PORNITON and initial analysis of more than 15,000 full-length
R. Pocon Matl. Acad Sci. U.S.A. 9916899-16903(2002);
R. PORNITON Acad Sci. U.S.A. 9916899-16903(2002);
R. PORNITON Acad Sci. U.S.A. 9916899-16903(2002);
R. PORNITON Acatulous Corp. Sci. U.S.A. 9916899-16903(2002);
R. Subcellular and Virial proteins
R. Carlandon Linds and Virial proteins
R. Carlandon Linds and Carlandon Cytoplasmic
R. Subcellular and Virial proteins
R. Subcellular and Virial statement is not removed a base by non-profit institution as a long as inspected by non-profit institutions and long R. Subcellular and P. R. Score 48; DB Subcellular and All Score 12; R. Score 48; DB Subcellular
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Search completed: October 14, 2003, 08:39:11 Job time: 11.8636 secs

108 TMEEASKKSYQFWDTQPVPKLGEVVNTHGPVEPDKDNIRQEPYTLPQGF 156

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB s Maximum DB s

Database

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Q9m9r8 arabidopsis
Q8m9r8 arabidopsis
Q8s9b0 brassica ca
Q23859 brassica ca
Q9saz7 brassica ca
Q9saz7 brassica ca
Q9znw9 brassica ca
                        039280 brassica ca
080351 raphanus sa
023843 brassica ol
039392 brassica ol
039924 drosophila
089924 drosophila
                                                                                                                                                    Q96jv0 homo sapien
Q95jr2 homo sapien
Q95jr3 cottolasion
Q95jr9 cottolasion
Q95jr0 octtolasion
Q95jr0 octtolasion
Q95jr0 octtolasion
Q95jr6 arabidopsis
Q97ap4 thermoplasm
Q81cq2 arabidopsis
           bifidobacte
                  09s412 actinobacil
  28ghm6 pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                       Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
Kangawa K., Eto T.;
"Adrenomedulin (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
SUDMITTED ADRENAL MEDULIA.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL. ABOSSIO1; BABS Adrenomedullin.
Pfan, PF02039; Adrenomedullin; I.
PRINTS; PR00801; ADRENOMEDULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovine; Bos.
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           28g3h2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 89.6%; Score 146; DB 6; Length 188; Local Similarity 90.3%; Pred. No. 3e-13; es 28; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20963 MW; 6102E69A756DCA86 CRC64;
                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
Q8GHM6
Q8G3H2
Q9S412
Q39280
O80351
O23843
                                                                                                                                            092NW6
096JV0
                                                                                  Q9M9R8
Q8S9B0
Q23859
Q23857
Q9SAZ7
Q98AT6
                                                                                                                                                                                                      0951T8
0958G9
09LJ66
097AP4
08LC02
                                                                                                                                                                                                                                                                                                                          Created)
                                                 Q39392
Q9MB87
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                    O9ZNW9
                                                                                                                                                                    0951T7
0951T9
094P28
0951U0
                                                                          QBMSUB
                                                                                                                                                            Q96JM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  100000
                                                                   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                 90
425
427
428
436
653
846
860
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                           1412
167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                Adrenomedullin.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                        Q95KP0
                                                                                                                                                                                                                                                                                                                                                          PBAM-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9TRZ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                      RESULT 1
Q95KP0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
Q9TRZ6
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qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8xe03 escherichia
Q23846 brassica ol
Q9seb5 hirschfeldi
O23849 brassica ca
Q9sbp2 raphanus ra
Q8sb2 brassica ol
Q8bb2 canorhabdi
Q9bia5 caenorhabdi
Q9bia9 caenorhabdi
Q9bia9 prassica na
Q23839 brassica na
Q23839 brassica na
Q23819 brassica na
Q23819 brassica na
Q8bCO51 mus musculu
                                                 October 14, 2003, 08:36:06; Search time 41.5682 Seconds (without alignments) 192.446 Million cell updates/sec
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Q9trz6 sus scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                  830525
  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                             163
1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                               830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM protein - protein search, using sw model
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Q8XA03
Q23846
Q9SEB5
Q23849
Q9SBP2
Q8S9B2
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056958
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Q8K0C1
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                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                      sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                   sp_invertebrate:*
sp_mammal:*
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sp_archeap:*
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seq length: 2000000000
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sp_bacteria:*
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sp_rodent:*
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                                                                                     US-09-931-700-3
                                                                                                                                                                                                                                                                   sp_fungi:*
sp_human:*
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189
430
367
421
373
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Match
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Score

Result Š. 34.48;

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11; Conservative
               Best Local Similarity Matches 11; Conserv
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SEQUENCE
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0
                                                                                                                                                                                                                                                         MEDLINE-96157714; PubMed-8576091; Ichiki Y. Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.; Ichiki Y., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.; Poistribution and characterization of immunoreactive adrenomedullin in porcine tissue, and isolation of adrenomedullin [26-52] and adrenomedullin [34-52] from porcine duodenum."; Is 18-757701995.

InterPro: IPR001710; Adrenomedullin.
PFINITS: PR00801; Adrenomedullin, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-0157-R7 / RIMD 0509952;
STRAIN-0157-R7 / RIMD 0509952;
MPDLINE-21156231; Pubmed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tamaka M., Tobe T., Hida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa Hi, Complete genome sequence of enterchemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Fosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 138; DB 6; Leus...
Pred. No. 5.2e-13;
--+-nes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B702A8F7387CF6D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B8DC7FA18D8B3D90 CRC64;
                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
ADRENOMEDULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l protein; Complete proteome.
189 AA; 21438 MW; B702A8F73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE005184; AAG54373.1; -. EMBL; AP002550; BAB33496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, C
01-MAR-2002 (TrEMBLrel. 20, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein 20078.
20078 OR ECSO073.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21438 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.78;
96.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3063 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 96.3
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 AA;
                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=83334;
                                                                                                                                                                                        NCBI_TaxID-9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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ACCOCCOS DE LA COMPANA COCCOS DE LA COCCOS DEL COCCOS DE LA COCCOS DEL COCCOS DE LA COCCOS DE LA
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DB 16; Length 189;

Score 58.5;

35.98;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pistil;
MEDLINE-21148766; PubMed-11254120;
Luu D.T., Hugues S., Passelegue E., Heizmann P.;
"Evidence for orthologous S-locus-related I genes in several genera of
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durachfeldia incana.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Hirschfeldia.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35.6%; Score 58; DB 10; Length 430; 25.6%; Pred. No. 4.6; Live 12; Mismatches 7; Indels 1
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 AA; 49149 MW; E76EC9219F8D9641 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: D85212: BAA21946.1; -
EMBL: D85212: BAA21946.1; -
InterPro; IPR001460; B_lectin.
InterPro; IPR003014; PAN.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR0060858; Slocus_glycop.
Ffam; PP01024; PAN: 1.
Pfam; PP00024; PAN: 1.
Pfam; PP00024; PAN: 1.
Pfam; PR00108; B_lectin; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM001473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
S glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QKLAHQIYQFTDKDKD-----NVAPRSKISPQGY 31
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
S-locus related (Fragment).
                    7;
                                                                                         4 KLAHQIYQFTD----KDKDNVAPRSKISPQG 30
Pred. No. 1.6;
9; Mismatches
                                                                                                                                                                                                                  430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 AA
                                                                                                                                                                                                                                           (TrEMBLrel. 05, Created) (TrEMBLrel. 05, Last
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                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                  Brassica oleracea (Cauliflower).
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                                                                                                                                                                                                                PRELIMINARY;
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les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3712;
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us-09-931-700-3.rspt

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receptor kinase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             368
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Best Local Similarity
The 12; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
hes 11; Conserv
                                                                                                                     SEQUENCE FROM N.A.
                                                              eurosids II; Brass.
NCBI_TaxID=109997;
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                                                                                                                                                                                                                    Brassicaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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NON_TER
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Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
"Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: Implications for the evolution and recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica campestis (Field mustard).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.

NCBI_TaxID=3711;
                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                              Score 56; DB 10; Length 367;
Pred. No. 7.6;
9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 431;
                                                                                                                                                                                                                                                                      9; Indels
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                                                                                                                                                                                         367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49227 MW; BED2FAFB8C3CD4B5 CRC64;
                                                                                                                                                                                                                                                                                                                                 232 QKLNYMVYNFTENSEDVAYTFRMTNKSIYSRLKISSEGF 270
                                                                                                                                                                                                                                                                                                      3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
BMBL: D85215; BAA21949.1; -.
InterPro: IPR001440; Blactin.
InterPro: IPR003609; Pan.app.
InterPro: IPR00858; Slocus_glycop.
Pfam; PF001453; Agglutinin; 1.
Pfam; PF00954; Slocus_glycop; 1.
SMART; SM00108; Blectin; 1.
SMART; SM00473; PAN.Ap; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.48; Score 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
          Mol. Gen. Genet. 264:735-745(2001).
EMBL; AF162909; AAF22268.1; -.
InterPro: IPR001480; B_lectin.
InterPro: IPR000858; Slocus_glycop.
Pfam; PF01453; Agglutinin; 1.
Pfam; PF00954; S_locus_glycop; 1.
SMARF; SM00108; B_lectin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                              ch 34.4%;
l Similarity 28.2%;
11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19, S-locus related (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.8%;
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Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                         367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 AA;
                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                       367
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Brassicaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mechanism.";
                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                              Query Match
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023849
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Raphanus raphanistrum subsp. raphanistrum.
Bukaryota, Vilidiphantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Raphanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brassica oleracea (Cauliflower).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          368 AA; 41672 MW; 1D455F6FB9B704D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 AA; 48015 MW; 835E29608FC9F160 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.7%; Score 55; DB 10; 28.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                                       Interpro: IPR001480; B_lectin.
Interpro: IPR001858; Slocus_glycop.
Pfam; PF00453; Agglutinin; 1.
SMART; SM00108; B_lectin; 1.
                                                                                                                                                                                                                                                    Mol. Gen. Genet. 264:735-745(2001).
EMBL; AF162905; AAF22264.1; -.
                                                                                                                                              TISSUE-Pistil;
MEDLINE-21148766; Pubmed=11254120;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhaditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .,
0
                                                                                                                                                                                                                                                               32.5%; Score 53; DB 5; Length 346; 40.0%; Pred. No. 19;
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Pred. No. 20,
7; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Du Z.;
"The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U41279; AAK31428.1; -.
HSSP; P23911; 108U.
                                                                                                                                                                                                        346 AA; 39688 MW; CF853F9CAF0B93B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41046 MW; D62561FC872C1158 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 41.0 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 AA
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                                                                                                                                                                                                                                                                                                                   7; Mismatches
                                                               WormPep; C17C3.1b; CE27071.
InterPro; IPR003703, Acyl_CoA_thio.
Pfam; PF02551; Acyl_CoA_thio; 2.
IIGRFAMS; TIGR00189; tesB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WormPep; C1703.1a; CE27070.
InterPro; IPR003703; Acyl_CoA_thio.
Pfam; PF02551; Acyl_CoA_thio; 2.
IIGRNAMS; IIGR00189; tesB; 1.
Hypothetical protein.
SEQUENCE 357 AA; 41046 MW; D6250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                       |::||::||::|
37 QEIAHKFFDFTELKKDSFSP 56
                                                                                                                                                                                                                                                                                                                                                                       3 QKLAHQIYQFTDKDKDNVAP 22
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        EMBL; U41279; AAK31429.1; -. HSSP; P23911; 108U.
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Best Local Similarity 40.00,
Best Local Similarity 60.00,
                                                                                                                                                                                                                                                                                      Best Local Similarity 40.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                              protein.
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                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                               Query Match
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Q8H0C3;
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ID 06
AC 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Mucleic Acids Res. 28:4317-4331(2000).

EMBL: APO01519; BAB07382.1; -.

InterPro; IPR001296; Glyco_trans_1.

Pfam, PF00534; Glycos_transf_1; 1.

Complete protecome.

SEQUENCE 373 AA; 42062 MW; OC67C2C98CBA4107 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis,
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=C-125 / JCM 9153;

MEDLINE-20512582; PubMed=11058132;

Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.1%; Score 54; DB 16; Length 373;
48.0%; Pred. No. 15;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.; "Direct Submission."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                      Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of C. elegans cosmid C17C3.";
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
227 QKLSYMMYNFTDNSEEVAYTFIMTNNSFYSRLKLSSEGY 265
                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TTEMBLrel. 17, Created)
01-JUN-2001 (TTEMBLrel. 17, Last sequence update)
01-JUN-2003 (TTEMBLrel. 23, Last annotation update)
01-MAR-2003 (TTEMBLrel. 23, Last annotation update)
C17C3-1.
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                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                          Lipopolysaccharide biosynthesis.
BH3663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.0%
Matches 12; Conservative
                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                  Q9K6R4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9BIA5
                                                                                                                                        Q9K6R4
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                                                                                 RESULT 9
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Q9BIA5

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056958
056958;
01-JUN-1998
                                            01-JUN-1998
01-JUN-2001
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Best Local S
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                                                                                                        Viruses;
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                                                                                                                                                                                                                                                                                                                                                                    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97352858; PubMed=9207151; Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.; Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.; "Striking sequence similarity in inter- and intra-specific comparisons of class I SLG alleles from Brassica oleracea and Brassica campestris: Implications for the evolution and recognition mechanism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Brāssicā oleracea (čauliflower).
Bukaryota; Vitidiplantae; Streeptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                        Brassica napus (Rape).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.9%; Score 52; DB 10; Length 428;
                                                                                                                                                                                                                                    DB 10; Length 430; 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                           9; Indels
                                                                                                                          SECUENCE FROM N.A. Odashima M., Okamoto S., Nishio T.; Odashima M., Okamoto S., Nishio T.; "Distribution of S haplotypes in Brassica napus."; Submitted (201-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AB086974; BAC53782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48724 MW; 18E04542C7293BEA CRC64;
                                                                                                                                                                                                              430 AA; 49065 MW; 60152ED337CD0928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKLSYMVYNFTENSEEVAYTFRMTNNSFYSRLKVSSDGY 267
                                                                                                                                                                                                                                                                                               230 QKLGYMVYNFTENSEEVAYTFRITNNSIYSRLKVSSEGF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 QKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                   3 OKLAHQIYQFTDKDKD------NVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).

EMBL; D85205; BAA21939.1; -
InterPro; IPR001480; B_lectin.

InterPro; IPR003699; Pan_app.

InterPro; IPR003698; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                          8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   428 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01453; Agglutinin; 1. Pfam; PF00954; S.locus_glycop; 1. SMART; SM00108; B_lectin; 1. SMART; SM00473; PAN_AP; 1.
                                 S-locus glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.2%;
                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05,
                                                                                                                                                                                                                              Query Match
Best Local Similarity 25.6%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 28.2
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                  430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3712;
                                                                                                     NCBI_TaxID=3708;
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NON_TER
SEQUENCE
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SEQUENCE
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023839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P. SELUGANA...
C. STRAIN=ATCC35047...
C. STRAIN=ATCC35047...
C. Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
C. Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
C. Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
C. Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
C. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
C. Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
C. Brant, BAB973931, BAB97300.1;
C. DR InterPro; IPR005194; Glyco_hydro_650.
C. DR InterPro; IPR005196; Glyco_hydro_650.
C. DR Pfam; PF03633; Glyco_hydro_650.
C. DR Pfam; PF03632; Glyco_hydro_650.
C. DR Pfam; PF03632; Glyco_hydro_650.
C. DR Pfam; PF03632; Glyco_hydro_650.
C. SEQUENCE 775 AA; 89700 MW; FB9760F02B220E56 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31.9%; Score 52; DB 2; Length 775; 36.0%; Pred. No. 65; 1. Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Indels
                                                                                                                                                                                                                                 dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 240:359-365(1998).

BEMBL: Y15176; CAA75476.1; -.

Interpro; IRPR002210; PV_capsid_L1.

Pfam; PF00500; late_protein_L1; 1.

PRINTS; PR00865; HPVCAPSIDL1.

PRODOM; PD00065; HPVCAPSIDL1.

PRODOM; P000674; PV_capsid_L1; 1.

SEQUENCE 507 AA, 56998 MW; 6F17589CC91004F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoanaerobacter brockii (Thermoanaerobium brockii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TVQKLAHQIYQFTD----KDKDNVAPRSKISPQG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              775 A.
507 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 AVRLYHYEDKEKNNIAKFKRFLPLG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AHQIYQFTDKDKDNVAPRSKISPQG 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                            E6, E7, E1, E2, E4, L2, and L1 genes
                                                         Created)
   PRT;
                                                                                                                                                                                                      Human papillomavirus type 80.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.9%;
38.2%;
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                                                   (TrEMBLrel. 06, (TrEMBLrel. 06, (TremBLrel. 17,
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Matches 13; Conservative
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   PRELIMINARY;
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=29323;
                                                                                                                                                                                                                                                                                        NCBI_TaxID=69987;
                                                                                                                                                                                                                                                                Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
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Search completed: October 14, 2003, 08:40:19 Job time: 44.5682 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31; Search time 20.4318 Seconds

(without alignments)

64.196 Million cell updates/sec

Title: US-09-931-700-3

Perfect score: 163
Sequence: 1 TWQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 328717 seqs, 42310858 residues
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

328717

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Issued\_Patents\_AA:\*

1: \cgn2\_6\ptodata1/1\iaa\5A\_COMB.pep:\*

1: \cgn2\_6\ptodata1/1\iaa\6A\_COMB.pep:\*

3: \cgn2\_6\ptodata1/1\iaa\6A\_COMB.pep:\*

4: \cgn2\_6\ptodata1/1\iaa\6B\_COMB.pep:\*

5: \cgn2\_6\ptodata1/1\iaa\Pep:\*

6: \cgn2\_6\ptodata1/1\iaa\Pep:\*

6: \cgn2\_6\ptodata1/1\iaa\Pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|           | Description              | 23,              | e,               | Sequence 14, Appl | σì    | 9     | ij               | Н                | 'n               | 'n     | <del></del> i    | H               | ις.             | ñ                | ě               | 'n               | 3,              | 4            | Sequence 8, Appli | 7,   | 'n            | 15,          | 'n      | Sequence 1, Appli | •             | equence 16, Appl | _           | Sequence 10, Appl |  |
|-----------|--------------------------|------------------|------------------|-------------------|-------|-------|------------------|------------------|------------------|--------|------------------|-----------------|-----------------|------------------|-----------------|------------------|-----------------|--------------|-------------------|------|---------------|--------------|---------|-------------------|---------------|------------------|-------------|-------------------|--|
|           | Desc                     | Sec              | Sec              | Sec               | Sec   | Sec   | Sec              | Sec              | Sec              | Sec    | Sec              | Sec             | Sec             | Sec              | Sec             | Sec              | Sec             | Se           | Sec               | Se   | Sec           | Se           | Se      | Se                | Se            | Se               | Se          | Sé                |  |
| SUMMAKIES | O.                       | US-09-070-504-23 | US-09-011-922A-3 | 09-011-           | 501-  | 501-  | US-09-280-501-11 | US-09-070-504-14 | US-08-233-389C-1 | 3-801- | US-08-486-596A-1 | US-09-004-713-1 | US-09-280-501-5 | US-08-233-389C-3 | US-08-801-863-3 | US-08-486-596A-3 | US-09-004-713-3 | -09-280-501- | -09-280-          | 9    | -09-280-501-3 | -09-070-504- | -09-280 | -09-280-501       | -09-280-501-1 | -280 - 501 - 1   | -09-280-501 | -09-280-501-1     |  |
|           | 1 DB                     |                  | 4                | 4                 | 4     |       |                  | m                |                  |        |                  |                 |                 |                  |                 | 3                | 8               | 4            | 0 4               | 4    | 8 4           | 0 3          | 7 4     | 6 4               | 3 4           | 1 4              | 3 4         | 3.4               |  |
|           | Length                   | 31               | 3]               | 33                | 3     | 38    | 4                | Š                | 18               |        |                  |                 |                 |                  |                 |                  |                 |              |                   |      |               |              |         |                   |               |                  |             |                   |  |
| ø         | Query<br>Match Length DB | 100.0            | 100.0            | 100.0             | 100.0 | 100.0 | 100.0            | 100.0            | 100.0            | 100.0  | 100.0            | 100.0           | 96.9            | 96.3             | 96.3            | 96.3             | 96.3            | 94.5         | 92.0              | 92.0 | 91.4          | 8.06         | 88.3    | 85.9              | 75.5          | 68.7             | 45.4        | 41.7              |  |
|           | Score                    | 163              | 163              | 163               | 163   | 163   | 163              | 163              | 163              | 163    | 163              | 163             | 158             | 157              | 157             | 157              | 157             | 154          | 150               | 150  | 149           | 148          | 144     | 140               | 123           | 112              | 74          | 89                |  |
|           | Result<br>No.            | ; r-1            | 7                | 9                 | 4     | S     | 9                | 7                | 8                | σı     | 10               | 11              | 12              | 13               | 14              | 15               | 16              | 17           | 18                | 19   | 20            | 21           | 22      | 23                | 24            | 25               | 26          | 27                |  |

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| Sequence 2, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 2465, A<br>Sequence 17, Appl<br>Sequence 2, Appl 11, Appl   |
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| US-09-011-922A-2 US-08-966-38B-4 US-09-18B-401-4 US-09-18B-404-4 US-09-281-2591A-24655 US-08-934-222-17 US-08-933-402-17 US-08-933-402-17 US-08-532-81B-17 US-08-532-81B-17 US-08-33-81B-17 US-09-331-402-17 US-08-331-402-17 US-08-331-402-17 US-08-331-402-17 US-08-331-402-17 US-08-331-402-17 US-08-34-23-17 US-08-34-23-17 US-08-34-23-17 US-08-380-380-380-380-380-380-380-380-380-  |
| 40000400000000000  |
| 13<br>775<br>775<br>775<br>775<br>775<br>100<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10<br>10   |
| 35.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0<br>37.0 |
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Gaps
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                                                                                                                                                        TITLE OF INVENTION: PERTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-APR-1998
CLASSIFICATION:
ATTORNEY/ASPRI INFORMATION:
NAME: MCCOLMACK, MyTR H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 163; DB 3;
100.0%; Pred. No. 2.4e-19;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                         ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180.00020101
                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                Sequence 23, Application US/09070504
Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Saha, Shankar
APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 612/305-1220
612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.8
Best Local Similarity 100.
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                55401
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RESULT 1
US-09-070-504-23
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Sequence 14, Application US/09011922A
Patent No. 6320022
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                                                                                                                                                                                                                                 Functional Role of Adrenomedullin (AM) and the Gene-Related Product (PAMP) in Human Pathology and Physiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.4e-19; ive 0; Mismatches 0; Indels
                                                                                                                     GENERAL INFORMATION:
APPLICANT: Cuttitta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: 7: Hook, William; Malsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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APPLICATION NUMBER: US/60/002,514
FILING DATE: 18 Aug-1995
FILING DATE: 18 Aug-1995
FILING DATE: 30-Aug-1995
FILING DATE: 30-Aug-1995
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
FILING DATE: 12-Mar-1996
FILING DATE: 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2026-4202US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REDABLE FORM:
MEDIUM TYBE: Floppy Disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3
                                                                                                                                                                                                                                                                                                                                                               DE: MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
                                                                              Sequence 3, Application US/09011922A
Patent No. 6320022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Leslie A. Serunian
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.(
Matches 31; Conservative
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TITLE OF INVENTION: Adre
TITLE OF INVENTION: Pro
TITLE OF INVENTION: Phys
NUMBER OF SEQUENCES: 17
CCRRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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STREET: 34
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                                  RESULT 2
US-09-011-922A-3
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STATE:
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RESULT 3 US-09-011-922A-14

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0
              APPLICANT: Cuttifta, Frank; Martinez,
APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
APPLICANT: Alfredo; Milliam; Walsh, Thomas; Grey,
APPLICANT: Karen; Macri, Charles
TITLE OF INVENTION: Functional Role of
TITLE OF INVENTION: Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 163; DB 4; Length 31; 100.0%; Pred. No. 2.4e-19; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic homolog of two-thirds of the intact AM peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,922A
FILING DATE: 17-Feb-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,514
FILING DATE: 18-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/002,936
FILING DATE: 30-Aug-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/60/013,172
FILING DATE: 12-Mar-1996
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
FILING DATE: 16-Aug-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2026-4202US3
                                                                                                                                                                                                                                              MORGAN & FINNEGAN, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cooper, Garth James Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 9, Application US/09280501; Patent No. 6440421; GENERAL INFORMATION: APPLICANT: Cooper, Garth James Smit
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible OPERATING SYSTEM: MS WORD 97
                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy Disk
IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leslie A. Serunian
                                                                                                                                                                                                                                                                    345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO FEATURE.
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                        RY: USA
10154-0053
GENERAL INFORMATION:
                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-011-922A-14
                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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US-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-070-504-14
                                                                                                                                       US-09-280-501-11
                                                                    LENGTH: 40
                                               SEQ ID NO 11
                                                                                            TYPE: PRT
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Sequence 6, Application US/09280501
| Sequence 6, Application US/09280501
| Patent No. 6440421
| SEPREAL INFORMATION
| APPLICANT: Corner, Garth James Smith
| APPLICANT: Corner, Jillian
| TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
| TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
| TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
| TITLE OF INVENTION: ADDRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
| FILE REFERENCE: 08987-00501
| CURRENT FILING DATE: 1999-03-30
| PRIOR PILING DATE: 1999-04-18
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Jillian
TITLE OF INVENTION: TREATHENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT FILING DATE: 1999-03-30
PRIOR PILING DATE: 1996-04-18
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN ACONISTS
CURRENT APPLICATION NUMBER: US/09/280,501
CURRENT APPLICATION NUMBER: US/03.30
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1999-04-18
NUMBER OF SEQ ID NGS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 163; DB 4; Length 38; 100.0%; Pred. No. 3.1e-19; tive 0; Mismatches 0; Indels
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Patent No. 6440421
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Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-6
                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-280-501-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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US-09-280-501-11
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LENGIH: 38
                                                                                                                                                                                                                                                         SEQ ID NO 9
LENGIH: 31
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                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                           Ouery Match 100.0%; Score 163; DB 4; Length 40; Best Local Similarity 100.0%; Pred. No. 3.3e-19; Matches 31; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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FILING DATE: 30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , DB 3;
4.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Mueting, Raasch & Gebhardt, P.A. STREET: 119 No. 6268474th Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 TVOKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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100.0%; Pred. No. 4.5
tive 0; Mismatches
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ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

~wenter: IBM PC compatible

~wenter: The PC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 14, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36,602
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 612/305-1220
TELEPRAX: 612/305-1228
INPORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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NAME: MCCormack, Myra H
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Smith, Derek D. APPLICANT: Saha, Shankar APPLICANT: Abel, Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.(
Watches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-09-070-504-14
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Length 185;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                          Query Match

100.0%; Score 163; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.1e-18;
Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 163; DB 2;
100.0%; Pred. No. 2.1e-18;
tive 0; Mismatches 0;
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NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 5HGN-5 DIVI
TELECOMMUNICATION INFORMATION:
TELEPERAK: (212) 596-9000
TELEFRAX: (212) 596-9000
TELEFRAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
                                              NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEFENNE: (212) 596-9000
TELEFAX: (212) 596-900
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: KITAMURA, KAZUO
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, HISAYUKI
APPLICANT: ETO, Tanenao
TILLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08486596A, Patent No. 5837823
                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
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Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-801-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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ZIP: 10020
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US-08-486-596A-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                 CARACTA TO THE LUCATION NUMBER: US/08/233,389C
FILING DATE: 26-APR-1994
CLASSIFICATION 530
ATTOREX/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/COCKET NUMBER: 27,794
REJERPHONE: (212) 596-900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08801863
Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGARA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: MATSUO, Hisayuki
APPLICANT: ETO, Tanenao
ITILE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
                    KITAMURA, Kazuo
KANGAWA, Kenji
MATSUO, Hisayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 10020
                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-233-389C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-801-863-1
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                                                                                                                                                                                                                                           STATE:
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96.3%; Score 157; DB 1; Length 188; 96.8%; Pred. No. 2e-17; ive 0; Mismatches 1; Indels
                                                                                                                         Length 30;
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                                                                                                                         96.9%; Score 158; DB 4; I 100.0%; Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 TYQKLAHQIYQFTDKDKDGVAPRSKISPQGY 146
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                                                                                                                                          100.0%; Preu. ....
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                                                                                                                                                                                                                                                   2 VQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSED: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: CURRENT APPLICATION DATA: CURRENT APPLICATION DATA: US/08/233,389C
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Patent No. 5830703
GENERAL INFORMATION:
APPLICANT: KANCHAW, Kenji
APPLICANT: MAUSUO, Hisayuki
APPLICANT: BOOGHOON:
APPLICANT: APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08233389C
Patent No. 5639855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F. P.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SH
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 188 amino acids
amino acid
                                                                                                                                                                                        30; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: 26-APF
CLASSIFICATION: 530
                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                          Best Local Similarity
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Best Local Similarity
Matches 30; Conserv
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US-08-801-863-3
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                                                           US-09-280-501-5
                                                                                                                         Query Match
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APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
TITLE OF INVENTION: ADDENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: U8/09/280,501
CURRENT APPLICATION NUMBER: 08/634,562
PRIOR APPLICATION NUMBER: 08/634,562
PRIOR FILING DATE: 1996-04-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,713 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 163; DB 2;
100.0%; Pred. No. 2.1e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET MUMBER: SHGN-5 DIVZ CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 TVQKLAHQIXQFTDKDKVAPRSKISPQGY 146
116 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: KIRAMURA, Kazuo
APPLICANT: KANGAMA, Kenji
APPLICANT: MATSOO, Hisayuki
APPLICANT: ETO, Tanenao
TITLE OF INVANTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6440421
                                                                                                                                                          Sequence 1, Application US/09004713 Patent No. 5910416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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US-09-280-501-5
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                                                                                               RESULT 11
US-09-004-713-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk

COMPUTER: THORY
MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC compatible
COMPUTER: THEN PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,863
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: HALEY Jr., James F.
REFIERANCE/DOCKET NUMBER: 27,794
REFIERANCE/DOCKET NUMBER: 27,794
REFIERANCE/DOCKET NUMBER: SHGN-5 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acids
TYPE: amino acids
TOPPLICATION
TOPPL
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/486,596A
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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APPLICANT: KITAMURA, Kazuo
APPLICANT: KANGAWA, Kenji
APPLICANT: KANGAWA, Kenji
APPLICANT: MATSUO, Hisayuki
APPLICANT: TO, Tanenao
TITLE OF INVENTION: ADRENOMEDULLIN
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
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NAME: HALEY Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: SHGN-5 DIVI
                                                                                                              ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
TITLE OF INVENTION: ADRENOMEDULLIN NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 30, Conservai
                                                                                                                                                 STREET: 1251 Av CITY: New York
                                                                                                                                                                                                                                                               USA
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ZIP: 10020
                                                                                                                                                                                                                        STATE: NI
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-486-596A-3
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October 14, 2003, 08:40:27 ; Search time 62 Seconds (without alignments) 80.564 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/MS07_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600653
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              600653 seqs, 161128416 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                   US-09-931-700-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                               Sednence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITALANDITOR

/cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US10\_NEM\_-UB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_NEM\_-PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

/cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*/cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*

|           | Description              | Sequence 3, Appli | Sequence 14, Appl | Sequence 23. Appl | Sequence 14. Appl | Segmence 2. Appli | Sequence 15. Appl | Seguence 2. Appli | Sequence 31. Appl | Sequence 4. Appli | Sequence 3547. Ap  | Sequence 8547. An  | Seguence 43882, A   | Sequence 570. App | Sequence 174. App | 41,              |
|-----------|--------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|--------------------|--------------------|---------------------|-------------------|-------------------|------------------|
| SUMMAKIES | ID                       | US-09-931-700-3   | US-09-931-700-14  | US-09-813-345-23  | US-09-813-345-14  | US-10-197-954-2   | US-09-813-345-15  | US-09-931-700-2   | US-10-427-631-31  | US-09-795-061-4   | US-10-128-714-3547 | US-10-128-714-8547 | US-09-864-761-43882 | US-10-102-806-570 | US-09-903-190-174 | US-09-738-269-41 |
|           | DB                       | 6                 | 6                 | 6                 | 6                 | 15                | 6                 | σ                 | 12                | 12                | 15                 | 15                 | OJ.                 | 15                | 12                | 12               |
|           | Suery<br>Match Length DB | 31                | 31                | 31                | 52                | 52                | 50                | 13                | 478               | 1745              | 984                | 1058               | 33                  | 327               | 131               | 809              |
| d         | ouery<br>Match           | 100.0             | 100.0             | 100.0             | 100.0             | 100.0             | 8.06              | 35.0              | 29.4              | 29.4              | 29.1               | 29.1               | 28.8                | 28.8              | 28.5              | 28.2             |
|           | Score                    | 163               | 163               | 163               | 163               | 163               | 148               | 57                | 48                | 48                | 47.5               | 47.5               | 47                  | 47                | 46.5              | 46               |
|           | Result<br>No.            | Н                 | 2                 | m                 | 4                 | Ŋ                 | 9                 | 7                 | 89                | 6                 | 10                 | 11                 | 12                  | 13                | 14                | 15               |

| Sequence 41, Appl Sequence 13, Appl Sequence 1, Appl Sequence 7130, Appl Sequence 7130, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 14, Appl Sequence 14, Appl Sequence 74, Appl Sequence |
|---|
| 14 US-10-023-437-41 11 US-09-791-279-219 12 US-10-359-3017-1 12 US-10-359-3017-1 12 US-10-032-585-7130 12 US-09-882-227-180 12 US-09-846-729A-17 12 US-10-441-667-3 12 US-10-441-667-14 12 US-10-441-667-14 15 US-10-441-667-14 15 US-10-441-667-14 15 US-10-219-667-14 12 US-10-219-068-7 12 US-10-219-068-7 12 US-10-219-068-7 12 US-10-219-068-7 13 US-10-219-068-7 14 US-10-219-068-7 15 US-10-219-068-7 16 US-10-219-68-7 17 US-10-219-68-7 18 US-10-219-68-7 19 US-10-219-68-7 11 US-10-219-7 12 US-10-219-7 13 US-10-219-7 14 US-10-219-7 15 US-10-219-7 16 US-10-219-7 17 US-10-219-7 18 US-10-219-7 19 US-10-219-53-7 19 US-10-219-53-7 11 US-10-219-53-7 12 US-10-219-53-7  |
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| 911120222222222222222222222222222222222   |

## ALIGNMENTS

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Sequence 3, Application US/09931700
Sequence 3. Application US/09931700
Sequence 3. Application US/09931700
Seatent No. US20020555151
GENERAL INFORMATION:
APPLICANT: MALILER, MAE JEAN
APPLICANT: WILLER, MAE JEAN
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WACRI, THOMAS
APPLICANT: WACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE REPRENCE: 2026-4202034
CURRENT FILING DATE: 2001-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072, OTHER INFORMATION: PreproAM (amino acids 116-146)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTREMY FILING DATE: 2010-08-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR PILING DATE: 1998-02-17
PRIOR PLING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1996-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
SOFTWARE: PATENTIN VEY: 2.1
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JS-09-931-700-3
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MARTINEZ, ALEREDO
APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KARLES
APPLICANT: MACRI, CHARLES
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physical Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physical Product (PAMP) in Human Pathology and
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Peptide, OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino OTHER INFORMATION: acid sequence representing two-thirds of the US-09-931-700-14
                                                                                               0;
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                                                   Length 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 163; DB 9; Length 31; 100.0%; Pred. No. 3.2e-17; tive 0; Mismatches 0; Indels
                                                                                               Indels
                                              Score 163; DB 9;
Pred. No. 3.2e-17;
                      100.0%; Scolution 100.0%; Pred. No. July 100.0%; Mismatches
                                                                                                                                                                      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202034
CURRENT PELLOATION NUMBER: US/09/931,700
CURRENT PELLING DATE: 2001-08-16
PRIOR PELLING DATE: 1998-02-17
PRIOR FILING DATE: 1996-08-16
PRIOR PILING DATE: 1996-08-18
PRIOR FILING DATE: 1996-08-30
PRIOR FILING DATE: 1996-08-30
PRIOR FILING DATE: 1996-08-30
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Patent No. US20020068814A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/09931700 Patent No. US20020055615A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Smith, Derek D. Saha, Shankar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                         Query Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: CUTTITIA, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Watches 31; Conserv
                                                                                                                                                                                                                                                                                US-09-931-700-14
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US-09-931-700-3
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 31;
STREET: 119 No. US20020068814Alth Fourth Street CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Mucting, Raasch & Gebhardt, P.A.
STREET: 119 No. U$20020068814A1th Fourth Street
CITY: Minneapolis
                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 163; DB 9;
100.0%; Pred. No. 3.2e-17;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 180.00020101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/813,345 FILING DATE: 20-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23;
                                                                                                                                                                                                                                                                                                                                                       NAME: MCCormack, Myra H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
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Patent No. US20020068814A1
GENERAL INFORMATION:
                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 31 amino acids
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Smith, Derek D.
Saha, Shankar
Abel, Peter W.
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
                                                                                                      USA
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                                                                              STATE: MN COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-813-345-14
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us-09-931-700-3.rapb

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NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
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US-09-931-700-2
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LENGTH: 13
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Publication No. US20030119021A1
GENERAL INFORMATION:
APPLICANT: Siddigl, Suhaib
APPLICANT: Siddigl, Suhaib
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: Compositions
FILE REFERENCE: 2474,32.305
CURRENT APPLICATION NUMBER: US/10/197,954
CURRENT FILING DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/316,019
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFTMARE: FastSEQ for Windows Version 4.0
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SADA, STANKAT
ADEL, PETER W.
TITLE OF INVENTION: PEPTIDE ANNAGONISTS OF CGRP-RECEPTOR
SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 52;
                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 163; DB 9; Length 52; Best Local Similarity 100.0%; Pred. No. 5.8e-17; Matches 31; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 No. US20020068814A1th Fourth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 163; DB 15;
100.0%; Pred. No. 5.8e-17;
clve 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                         1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                    22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 14:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/09813345
Patent No. US20020068814A1
GENERAL INFORMATION:
                                                            INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 52 amino acids
                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Smith, Derek D.
                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo Sapien
US-10-197-954-2
                                                                                                                                                                                                                                US-09-813-345-14
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LENGIH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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Gaps
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                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           NAME: MCCOTMACK, MYTA H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                           APPLICATION NUMBER: US/09/813,345
                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                               FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 50 amino acids
                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS
                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Flopp
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 87.13
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
               STATE: MN
COUNTRY: USA
ZIP: 55401
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RESULT 7
US-09-931-700-2
Sequence 2, Application US/09931700
Patent No. US2020055615A1
Sequence 2, Application US/09931700
Patent No. US2020055615A1
SEQUENCE 3. PAPELICANT: CUTITITA, FRANK
APPLICANT: UNEWATION:
APPLICANT: MARILIER, AME JEAN
APPLICANT: MILLER, AME JEAN
APPLICANT: MAGNETH, EDWARD J.
APPLICANT: MAGNETH, EDWARD J.
APPLICANT: MAGNETH, EDWARD J.
APPLICANT: GREY, KAREN
APPLICANT: GREY, KAREN
APPLICANT: PROME GREY, RANEN
APPLICANT: PROME JEAN
APPLICANT: PRICE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202044
CURRENT APPLICATION NUMBER: US/09/931,700
PRIOR FILING DATE: 1996-08-16
PRIOR FILING DATE: 1996-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-18
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LENGTH: 1745
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                                                                                                                                                                                        0
                                       OTHER INFORMATION: Description of Artificial Sequence: Peptide, OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches 12; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TVQKLAHQIYQFTD------KDKDNVAPRSKISPQGY 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.4%; Score 48; DB 12; Length 478; 24.5%; Pred. No. 81;
                                                                                                                                            Length 13;
                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: GenBank ID No. US20030175923A1 g2443814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 4, Application US/09795061
; Publication No. US20030166842A1
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Daniel S
; APPLICANT: Imamura, Yasutada
; FILE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
; FILE BEFERRUCE: 960296.96781
; CURRENT APPLICATION NUMBER: US/09/795,061
; CURRENT FILING DATE: 2001-02-26
; NOWERR OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: INCYTE CORPORATION; TANG, Y. TOM;
APPLICANT: INCYTE CORPORATION; TANG, Y. TOM;
APPLICANT: INCYTE CORLEY, Neil C.; GUEGLER, Karl J.;
APPLICANT: BADGHN, Marlah R.; LAL, Preeti G.;
APPLICANT: YUE, HENCY: HILLMAN, Jennifer L.;
APPLICANT: AZIMZAI, Yalda
ITITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
ITITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592-1 DIV
CURRENT APPLICATION NUMBER: US/10/427,631
CURRENT FILING DATE: 2003-04-29
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR PLING DATE: 1999-09-09
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-10
PRIOR PLING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
PRIOR FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGRAM
                                                                                                                                         DB 9;
0.06;
                                                                                                                                Query Match
35.0%; Score 57; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Sequence 31, Application US/10427631 Publication No. US20030175923A1 GENERAL INFORMATION:
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 24.5:
Matches 12; Conservative
                                                                                                                                                                                                                                                  4 HQIYQFTDKD 13
                                                                                                                                                                                                                         7 HQIYQFIDKD 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-427-631-31
                                                                                      US-09-931-700-2
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LENGIH: 47
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SEQ ID NO 4
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Sequence 3547, Application US/10128714

Publication No. US20030119013A1

GENERAL INFORMATION:

APPLICANT: Jiang, Bo

APPLICANT: Jishkoff, Daniel

APPLICANT: Tishkoff, Daniel

APPLICANT: Enamidalo, Carlos

APPLICANT: Lemieux, Sebastien M

TITLE OF INVENTION: Methods of Use

TITLE OF INVENTION: Methods: US 60/285,697

PRIOR APPLICATION NUMBER: US 60/285,890

PRIOR APPLICATION NUMBER: US 60/303,899

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: US 60/316,362

PRIOR APPLICATION NUMBER: US 60/316,362

PRIOR FILING DATE: 2001-08-31

NUMBER OF SEO ID NOS: 8603

SOFTWARE: PARTENTIN VETSION 3.1

SENTWARE: PARTENTIN VETSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Exoshkin, Alexey M
APPLICANT: Exoshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
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                                                                               29.4%; Score 48; DB 12; Length 1745; 53.3%; Pred. No. 3.6e+02; Live 4; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29.1%; Score 47.5; DB 15; 27.5%; Pred. No. 2.2e+02; tive 10; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QKLAHQIYQFTDK-------DKDNVAPRSKISPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Aspergillus fumigatus US-10-128-714-3547
                                                                                                                                                                                                                            | ||:|| : ::|||
223 DCDNLAPAATVAPQG 237
                                                                                                                                                                                          16 DKDNVAPRSKISPQG 30
                                                  Query Match
Best Local Similarity 53.3%
"Thes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
; ORGANISM: Homo sapiens US-09-795-061-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                       RESULT 10
US-10-128-714-3547
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                                                                                                                                                                                                                                                                          OTHER INFORMATION: MAP TO AC005079.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN BARIA. = 0.94

OTHER INFORMATION: EXPRESSED IN BOUB MARROW, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.69

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69

US-09-864-761-43882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 570, Application US/10102806
Fublication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALOSPICA.
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PATCHTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.8%; Score 47; DB 15; Length 327; 41.4%; Pred. No. 73;
ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.8%; Score 47; DB 9; Length 33; 62.5%; Pred. No. 5.3; 1.1ve 1; Mismatches 5; Indels
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 43882
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APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TILLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET.021A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 KLAHQI-YQFIDKDKDNVAPRSKISPQGY 31
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; Publication No. US20030162176A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VQKLAHQIYQFTDKDK 17
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Best Local Similarity 62.5
Matches 10; Conservative
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Best Local Similarity 41.4*
Matches 12; Conservative
                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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29.1%; Score 47.5; DB 15; Length 1058;
Best Local Similarity 27.5%; Pred. No. 2.4e+02;
Matches 11; Conservative 10; Mismatches 6; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 QEMMVEIFXYIDRVVNMVRPRKLIMIAVDGVAPRAKMNQQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DKDNVAPRSKISPQ 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCI/US01/00666
                          PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR PELING DATE: 2001-06-05
PRIOR PELING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR PLING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR PELING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00663
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PRIOR APPLICATION NUMBER: US 60/207,456
    PRIOR APPLICATION NUMBER: US 60/285,697
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43882, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 QKLAHQIYQFTDK------
                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8547
                                                                                                                                                                                                                                                                 SOFTWARE: Patentin version 3.1 SEQ ID NO 8547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-01-30
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US-09-864-761-43882
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Sequence 41, Application US/09738269
Sequence 41, Application US/09738269
GENERAL INFORMATION:
JAPPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: STEMKE-HALE, KATHERINE
APPLICANT: KATHERINE
APPLICANT: KATHERINE
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
TITLE OF INVENTION: MCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
TITLE OF INVENTION: CHLAMYDIA PSITTACI
FILE REFERENCE: UTSD:659
CURRENT APPLICATION NUMBER: US/09/738,269
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 61
SOFTMAKE: PATENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                   PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: BARLIER FILING DATE: 1998-02-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: BARLIER FILING DATE: 1998-08-10
PRIOR FILING DATE: BARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PALENT.PM
SEQ ID NO 174
LENGTH: 131
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28.5%; Score 46.5; DB 12; Length 131;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 8; Indels 9,
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28.2%; Score 46; DB 12; Length 608;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: 40,41,43,60,70,76,82,86,105,107; OTHER INFORMATION: Xaa = any one of the twenty amino acids US-09-903-190-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 IQKLAXQFVXLNLVYETIDK---HLSPDGQYXPXDY 129
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CURRENT APPLICATION NUMBER: US/09/903,190 CURRENT FILING DATE: 2001-07-11
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US-09-738-269-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: SIGNAL LOCATION: -20..-1 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: UNSURE
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US-09-738-269-41
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LENGTH: 608
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Search completed: October 14, 2003, 08:53:17

Job time : 63 secs

Perfect score:

Sequence:

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Scoring table:

Searched:

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Database :

Sequence 2, Appliance 195, Appliance 14, Appliance 14, Appliance 17, App

Sequence 14, Appl Sequence 6, Appli

Seguence

Seguence

Sequence

Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 148, App Sequence 12482, A Sequence 12482, A

Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli

Sequence 3

Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence 148, App Sequence 406, App

Sequence 5, Appli

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US-09-657-276-938

US-09-931-700-3

US-09-931-700-14

US-09-931-700-14

US-09-931-700-14

US-08-634-562-16

US-08-634-562-16

US-08-634-562-11

PCT-USO2-22821-2

US-09-623-548A-935

US-09-657-276-935

US-09-613-345-14

VS-10-10-36-135-124

US-09-724-676-63615

US-08-6453-050-12481

US-08-60-456-412-12481
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6 US-10 018 924-2
6 US-10 -364-889-6
2 US-60 -440-0689-6
2 US-60 -453-050-12482
2 US-60 -453-135-12482
2 US-60 -466-412-12482
2 US-60 -466-412-12482
8 US-10 -206-021-406
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US-08 -634-552-5
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US-10-030-298-4
US-08-634-562-4
US-09-475-158A-31
US-08-634-562-8
US-08-634-562-3
US-08-634-562-3
US-09-623-548A-944
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US-09-813-345-15
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OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08634562
GENERAL INFORMATION:
APPLICANT: COY, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Reid, Ian Reginald
APPLICANT: Rooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISOI
TITLE OF INVENTION: WITH ADRENOMEDULIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson P.C. 225 Franklin Street
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                      (without alignments)
69.629 Million cell updates/sec
                                                                                                                                             October 14, 2003, 08:38:52; Search time 405.114 Seconds
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22: /ggn2_6/ptodata/1/paa/US091_COMB.pep:*
22: /ggn2_6/ptodata/1/paa/US091_COMB.pep:*
23: /ggn2_6/ptodata/1/paa/US091_COMB.pep:*
24: /ggn2_6/ptodata/1/paa/US091_COMB.pep:*
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/cgn2_6/ptodata/1/paa/US102_COMB.pep:*
/cgn2_6/ptodata/1/paa/US103_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /ptodata/1/paa/US100_COMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ptodata/1/paa/US104_COMB.pep:*
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                            163
1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΩI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                     US-09-931-700-3
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163

No. Result

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USA
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US-09-813-345-23
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APPLICANT: CONJUGNEM, INC.

APPLICANT: Bridon, Dominique

APPLICANT: Miner, Peter

APPLICANT: Miner, Peter

APPLICANT: Holmes, Darren

TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM

TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD

FILE REFERENCE: 2110

CURRENT APPLICATION NUMBER: US/09/623,548A

PRIOR APPLICATION NUMBER: 60/134,406

PRIOR PLILNG DATE: 1999-05-10

PRIOR PLILNG DATE: 1999-05-10

PRIOR PLILNG DATE: 1999-05-10

PRIOR FILING DATE: 1999-05-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 163; DB 10;
100.0%; Pred. No. 1.3e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 163; DB 20; 100.0%; Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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                                                                   AFFILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGIGTRATION NUMBER: 34,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
APPLICATION NUMBER: US/09/634,562
FILING DATE: 18-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 938, Application US/09623548A GENERAL INFORMATION:
                                                                                                                                                          REFERENCE/DOCKET NUMBER: 088
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELERAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                               TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                    31 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear;
; MOLECULE TYPE: peptide
US-08-634-562-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Conjuchem, Inc.
                                                                                                                                                                                                                                                                                                                      amino acid
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LENGTH: 31
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RESULT 3

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APPLICANT: CONJUCHEM, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Holmes, Darren
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TIILE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
TITLE OF INVENTION: COMPONENTS
CURRENT APPLICATION NUMBER: 60/134,406
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR PILING DATE: 1999-10-16
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PATENTIN VEF. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide
US-09-657-276-938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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COMPUTER READABLE FORM:
MEDIOM TYPER: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: CURROWN>
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TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-REC SUPERFAMILY AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Mueting, Raasch & Gebhardt, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 163; DB 20;
100.0%; Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MCCORMACK, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TVQKLAHQIYQFTDKDKDKNVAPRSKISPQGY 31
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CITY: Minneapolis
Sequence 938, Application US/09657276 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23, Application US/09813345 GENERAL INFORMATION:
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Best Local Similarity 100.C
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Query Match
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APPLICANT: MILLER, MAE JEAN
APPLICANT: MILLER, ME JEAN
APPLICANT: MILLER, ME JEAN
APPLICANT: WISWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: WALSH, THOMAS
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Physiology
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202054
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 100.0%; Score 163; DB 24; l Similarity 100.0%; Pred. No. 1.3e-17; 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                             1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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CURRENT PELING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 09/011,922

PRIOR FILING DATE: 1908-02-17

PRIOR FILING DATE: 1996-08-16

PRIOR PILING DATE: 1996-08-16

PRIOR PILING DATE: 1996-08-16

PRIOR PILING DATE: 1996-03-12

PRIOR PELING DATE: 1996-03-12

PRIOR PELING DATE: 1996-03-12

PRIOR PELING DATE: 1995-08-30

PRIOR FILING DATE: 1995-08-30

PRIOR FILING DATE: 1995-08-30

PRIOR FILING DATE: 1995-08-31

SOFTWARE: PATENTING DATE: 1995-08-31

SOFTWARE: PATENTING DATE: 1995-08-31

SOFTWARE: PATENTING DATE: 1995-08-38
                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-09-931-700-14
; Sequence 14, Application US/09931700
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09931700 GENERAL INFORMATION:
                                                               LENGTH: 31 amino acids
TELEFAX: 612/305-1228
                                                                                     TYPE: amino acid
STRANDEDNESS: single
              INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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US-09-931-700-3
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                  APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KARENS
APPLICANT: GREY, KARENS
APPLICANT: GREY, CHARLES
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Grey, Grey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
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GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Cooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
TITLE OF INVENTION: WITH ADRENOMEDULLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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SOFTWARE: FastSEQ for Windows Version 2.0b
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                                                                                                                                                                                                                                                                                                                                                                                                            HILL REFERENCE: 2026 4202034
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-03-12
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
PRIOR FILING DATE: 1995-08-30
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APPLICATION NUMBER: US/08/634,562
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MARTINEZ, ALFREDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 31
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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ZIP: 02110-2804
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                                              1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
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               0; Mismatches
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PRIOR PILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SEQ ID NO 935
LENGTH: 52
                                                                                                                                                                            ; Sequence 2, Application PC/TUS0222821
; GENERAL INFORMATION:
                                                                                                                                                                                                                 APPLICANT: HK Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 31; Conservative 0
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ORGANISM: Artificial Sequence
FEATURE:
         31; Conservative
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US-09-623-548A-935
                                                                                                                                       RESULT 9
PCT-US02-22821-2
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LENGIH: 52
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           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COY, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Coper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
TITLE OF INVENTION: WITH ADRENOMEDULLIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163; DB 10;
Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows 95
OCTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,562
FILING DATE: 18 - APR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           1 TVQKLAHQIYQFIDKDKDNVAPRSKISPQGY 31
                       TUCKNET/ANDRA.
TSAO, T. ROCKY
REGISTRATION NUMBER: 34,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08987/002001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08634562 GENERAL INFORMATION:
                                                                     REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Tsao, Y. Rocky
REGISTRATION NUMBER: 34,053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                    LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-634-562-6
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.C
                                                                                                                              TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ZIP: 02110-2804
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US-08-634-562-11
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APPLICANT: Siddigi, Subalb
APPLICANT: Siddigi, Subalb
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
FILE REFERENCE: 24743-2305
CURRENT APPLICATION NUMBER: PCT/US02/22821
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 149
SOFFWARE: FastSEQ for Windows Version 4.0
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| Sequence 935, Application US/09623548A
| GENERAL INFORMATION:
| APPLICANT: Codyudhem, Inc.
| APPLICANT: Codyudhem, Inc.
| APPLICANT: Milner, Peter
| APPLICANT: Milner, Peter
| APPLICANT: Thibaudeau, Karen
| APPLICANT: Thibaudeau, Karen
| TITLE OF INVENTION: PROFECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
| TITLE OF INVENTION: COMPONENTS
| FILLE REFERENCE: 2110
| CURRENT APPLICATION NUMBER: US/09/623,548A
| PRINCE APPLICATION NUMBER: 60/134,406
| PRINCE APPLICATION NUMBER: 60/134,406
      Gaps
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; Pred. No. 2.5e-17;
0; Mismatches 0; Indels
Indels
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us-09-931-700-3.rapm

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MEDIUM TYPE: Floppy disk
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; GENERAL INFORMATION:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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Matches 31; Conservative
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US-10-197-954-2
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LENGTH: 52
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APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Dominique
APPLICANT: Bridon, Alan
APPLICANT: Milner, Peter
APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR APPLICATION NUMBER: 60/133,406
PRIOR APPLICATION NUMBER: 60/153,406
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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                                                                                      Length 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 52;
                                                                                                                              Indels
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ADDRESSE: Mueting, Raasch & Gebhardt, P.A.
STREET: 119 North Fourth Street
                                                                                  ; Score 163; DB 20;
; Pred. No. 2.5e-17;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 163; DB 20;
100.0%; Pred. No. 2.5e-17;
tive 0; Mismatches 0;
                                                                                                                                                           1 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 31
                                                                                                                                                                                     22 TVQKLAHQIYQFTDKDKDNVAPRSKISPQGY 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                    Sequence 935, Application US/09657276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09813345
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
                                                                                  100.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 23
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                                                                         Query Match 100.0
Best Local Similarity 100.0
Matches 31; Conservative
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Matches 31; Conservative
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COUNTRY: USA
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                                        US-09-623-548A-935
                                                                                                                                                                                                                                                            RESULT 11
US-09-657-276-935
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LENGTH: 52
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APPLICANT: Siddigi, Suhaib
APPLICANT: Little, Daniel
APPLICANT: Little, Daniel
TITLE OF INVENTION: Capture Compounds, Collections Thereof
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
TITLE OF INVENTION: Compositions
FILE REPERBNOG: 2473-2305
CURRENT PILITIG DATE: 2002-07-16
PRIOR APPLICATION NUMBER: 60/306,019
PRIOR PILITING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/314,123
PRIOR PILITING DATE: 2001-08-21
PRIOR FILING DATE: 2001-08-21
PRIOR FILING DATE: 2002-03-11
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
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                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCCOLMACK, MYTA H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEPHONE: 612/305-1220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT: Moll, Gert N.
APPLICANT: Leenhouts, Cornells J.
TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
FILE REFERENCE: 2183-5673
CURRENT APPLICATION NUMBER: US/10/360,101
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: EP 02077060.8
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 309
SOFTWARE: Patentin version 3.1
SEQ ID NO 74
LENGTH: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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100.0%; Score 163; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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TITLE OF INVENTION: Variants of alternative splicing
TITLE REFERENCE: 12918.1.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
UURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 163; DB 29; Best Local Similarity 100.0%; Pred. No. 2.5e-17; Matches 31; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TVQKLAHQIYQFIDKDKDNVAPRSKISPQGY 31
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ORGANISM: Homo sapiens
US-09-724-676-63615
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